GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:14:29 ; Search time 5216.6 Seconds
(without alignments)
9953.801 Million cell updates/sec

Title: US-10-763-400-1
Perfect score: 1198
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		1198	100.0	1198	6	AR175479	AR175479 Sequence
2	c	1198	100.0	1198	6	AR175480	AR175480 Sequence
3		1198	100.0	1198	6	AX074287	AX074287 Sequence
4	c	1198	100.0	1198	6	AX074289	AX074289 Sequence
5		1198	100.0	1198	6	AX101304	AX101304 Sequence
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8		1186.8	99.1	1198	6	I09686	I09686 Sequence 3
9		1144.8	95.6	1174	6	AR123794	AR123794 Sequence
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16		774	64.6	774	6	AR175481	AR175481 Sequence
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18		773	64.5	773	6	AR219964	AR219964 Sequence
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ALIGNMENTS

RESULT 1
AR175479
LOCUS AR175479 1198 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6309832.
ACCESSION AR175479
VERSION AR175479.1 GI:17916778
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 1198)
AUTHORS Frank,G.R., Porter,J.P., Rushlow,K.E. and Wassom,D.L.
TITLE Method to detect IgE
JOURNAL Patent: US 6309832-A 1 30-OCT-2001;
FEATURES Location/Qualifiers

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  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
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Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
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RESULT 2
AR175480/c
LOCUS       AR175480                1198 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 3 from patent US 6309832.
ACCESSION   AR175480
VERSION     AR175480.1  GI:17916779
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1198)
  AUTHORS   Frank,G.R., Porter,J.P., Rushlow,K.E. and Wassom,D.L.
  TITLE     Method to detect IgE
  JOURNAL   Patent: US 6309832-A 3 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .1198
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ORIGIN

  Query Match             100.0%;  Score 1198;  DB 6;  Length 1198;
  Best Local Similarity   100.0%;  Pred. No. 5e-266;
  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
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Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
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Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
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RESULT 3
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DEFINITION  Sequence 1 from Patent WO0104310.
ACCESSION   AX074287
VERSION     AX074287.1  GI:12710474
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Weber,E.R., Wood,K.V. and Hall,M.P.
  TITLE     Fc epsilon receptor-luminescence inducing protein chimeric nucleic
            acid molecules, fusion proteins and uses thereof
  JOURNAL   Patent: WO 0104310-A 1 18-JAN-2001;
            Heska Corporation (US) ; PROMEGA CORPORATION (US)
FEATURES             Location/Qualifiers
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ORIGIN
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  Query Match          100.0%;  Score 1198;  DB 6;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 5e-266;
  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
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Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198


RESULT 4
AX074289/c
LOCUS       AX074289               1198 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 3 from Patent WO0104310.
ACCESSION   AX074289
VERSION     AX074289.1  GI:12710476
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Weber,E.R., Wood,K.V. and Hall,M.P.
  TITLE     Fc epsilon receptor-luminescence inducing protein chimeric nucleic
            acid molecules, fusion proteins and uses thereof
  JOURNAL   Patent: WO 0104310-A 3 18-JAN-2001;
            Heska Corporation (US) ; PROMEGA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .1198
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1198;  DB 6;  Length 1198;
  Best Local Similarity   100.0%;  Pred. No. 5e-266;
  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1198 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 1139

Qy          61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1138 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 1079

Qy         121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1078 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 1019

Qy         181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1018 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 959

Qy         241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         958 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 899

Qy         301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         898 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 839

Qy         361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         838 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 779

Qy         421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         778 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 719

Qy         481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         718 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 659

Qy         541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         658 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 599

Qy         601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
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Db         598 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 539

Qy         661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
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Db         538 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 479

Qy         721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
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Db         478 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 419

Qy         781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         418 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 359

Qy         841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
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Db         358 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 299

Qy         901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         298 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 239

Qy         961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         238 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 179

Qy        1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         178 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 119

Qy        1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         118 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 59

Qy        1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          58 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1


RESULT 5
AX101304
LOCUS       AX101304               1198 bp    DNA     linear   PAT 10-APR-2001
DEFINITION  Sequence 7 from Patent WO0121816.
ACCESSION   AX101304
VERSION     AX101304.1  GI:13620094
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kinet,J.P., Donnadieu,E., Jouvin,M.H., Cookson,W. and Moffatt,M.F.
  TITLE     Modulation of ige receptor cell surface expression
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  JOURNAL   Patent: WO 0121816-A 7 29-MAR-2001;
            ISIS INNOVATION LIMITED (GB) ; Beth Israel Deaconess Medical
            Center, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1198
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1198;  DB 6;  Length 1198;
  Best Local Similarity   100.0%;  Pred. No. 5e-266;
  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
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Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
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Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
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Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
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Db       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198


RESULT 6
AX335621
LOCUS       AX335621                1198 bp    DNA     linear   PAT 09-JAN-2002
DEFINITION  Sequence 6130 from Patent WO0194629.
ACCESSION   AX335621
VERSION     AX335621.1  GI:18126340
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
            Horrigan,S., Soppet,D.R. and Weaver,Z.
  TITLE     Cancer gene determination and therapeutic screening using signature
            gene sets
  JOURNAL   Patent: WO 0194629-A 6130 13-DEC-2001;
            Avalon Pharmaceuticals (US)
FEATURES             Location/Qualifiers
     source          1. .1198
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             100.0%;  Score 1198;  DB 6;  Length 1198;
  Best Local Similarity   100.0%;  Pred. No. 5e-266;
  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
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Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
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Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
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Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
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Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
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Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
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Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
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Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
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Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198


RESULT 7
HSFCERI
LOCUS       HSFCERI                 1198 bp    mRNA    linear   PRI 21-MAR-1995
DEFINITION  Human mRNA for high affinity IgE receptor alpha-subunit (FcERI).
ACCESSION   X06948
VERSION     X06948.1  GI:31317
KEYWORDS    FcERI gene; IgE receptor alpha-subunit.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1198)
  AUTHORS   Kochan,J., Pettine,L.F., Hakimi,J., Kishi,K. and Kinet,J.P.
  TITLE     Isolation of the gene coding for the alpha subunit of the human
            high affinity IgE receptor
  JOURNAL   Nucleic Acids Res. 16 (8), 3584 (1988)
  MEDLINE   88233953
   PUBMED   2967464
REFERENCE   2  (bases 1 to 1198)
  AUTHORS   Kochan,J.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-FEB-1988) Kochan J. P., Hoffman-La Roche, Dept
            Molecular Genetics, 340 Kingsland, Nutley, New Jersey 07110
COMMENT     *source cell line=KU812; library=lambda gt11 cDNA.
FEATURES             Location/Qualifiers
     source          1. .1198
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="pLJ587 & pLJ663"
     CDS             107. .880
                     /note="unnamed protein product; precursor (AA -25 to 232)"
                     /codon_start=1
                     /protein_id="CAA30025.1"
                     /db_xref="GI:31318"
                     /db_xref="GOA:P12319"
                     /db_xref="SWISS-PROT:P12319"
                     /translation="MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKG
                     ENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESE
                     PVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHN
                     ISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAV
                     DTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN"
     sig_peptide     107. .181
                     /note="put. signal peptide (AA -25 to -1)"
     mat_peptide     182. .877
                     /product="mature IgE receptor (AA 1-232)"
     misc_feature    182. .718
                     /note="put. extracellular domain"
     misc_feature    719. .778
                     /note="put. transmembrane region"
     misc_feature    779. .877
                     /note="put. cytoplasmic tail"
ORIGIN

  Query Match           100.0%;  Score 1198;  DB 9;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 5e-266;
  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
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Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
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Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
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Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
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Qy         481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy         541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
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Db         541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy         601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy         661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
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Db         661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy         721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780

Qy         781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
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Db         781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy         841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
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Db         841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy         901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
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Db         901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy         961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
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Db         961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy        1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
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Db        1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy        1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy        1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
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RESULT 8
I09686
LOCUS       I09686                  1198 bp    DNA     linear   PAT 02-DEC-1994
DEFINITION  Sequence 3 from Patent WO 9004640.
ACCESSION   I09686
VERSION     I09686.1  GI:587606
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1198)
  AUTHORS   Kinet,J.-P. and Metzger,H.
  TITLE     cDNAs CODING FOR THE gamma SUBUNIT OF THE HIGH-AFFINITY RECEPTOR
            FOR IMMUNOGLOBULIN E
  JOURNAL   Patent: WO 9004640-A 3 03-MAY-1990;
FEATURES             Location/Qualifiers
     source          1..1198
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN
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  Query Match             99.1%;  Score 1186.8;  DB 6;  Length 1198;
  Best Local Similarity   99.4%;  Pred. No. 1.9e-263;
  Matches 1191;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy           1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy          61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy         121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
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Db         121 GGAATCCCCTACTCTACTCTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy         181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
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Db         181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy         241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
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Qy         301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
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Db         301 CCACAATGGGAGGCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy         361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy         421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy         481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy         541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
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Db         541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy         601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
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Db         661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy         721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
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Qy         781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
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Db         781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCACGAAAGGCTTCAGACT 840

Qy         841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
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Db         841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy         901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
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Qy         961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
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Qy        1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
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              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGCCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
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Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       1141 TATAAAACCATGTAACAGAATCCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198


RESULT 9
AR123794
LOCUS       AR123794                1174 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 10 from patent US 6171803.
ACCESSION   AR123794
VERSION     AR123794.1  GI:14109155
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1174)
  AUTHORS   Kinet,J.Pierre.
  TITLE     Isolation, characterization, and use of the human .beta. subunit of
            the high affinity receptor for immunoglobulin E
  JOURNAL   Patent: US 6171803-A 10 09-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .1174
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             95.6%;  Score 1144.8;  DB 6;  Length 1174;
  Best Local Similarity   99.7%;  Pred. No. 9.6e-254;
  Matches 1157;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
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Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
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Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
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Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
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Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
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Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
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Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
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Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
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Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
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Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
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Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db       1081 GAATGAATAGATTCATTTATTAGCA-TTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1139

Qy       1141 TATAAAACCATGTAACAGAA 1160
              ||||||||||||||| | ||
Db       1140 TATAAAACCATGTAAAAAAA 1159


RESULT 10
HUMMCIAA
LOCUS       HUMMCIAA                1081 bp    mRNA    linear   PRI 11-JUN-1993
DEFINITION  Human mast cell IgE receptor alpha-chain.
ACCESSION   J03605
VERSION     J03605.1  GI:187449
KEYWORDS    immunoglobulin-like sequence; receptor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1081)
  AUTHORS   Shimizu,A., Tepler,I., Benfey,P.N., Berenstein,E.H.,
            Siraganian,R.P. and Leder,P.
  TITLE     Human and rat mast cell high-affinity immunoglobulin E receptors:
            characterization of putative alpha-chain gene products
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 85 (6), 1907-1911 (1988)
  MEDLINE   88158102
   PUBMED   2964640
COMMENT     Original source text: Human mast cell line KU812, cDNA to mRNA,
            clone pAS-h-IgER-110B.
            Computer-readable copy of sequence in [1] kindly provided by
            P.Leder, 08-FEB-1988.
FEATURES             Location/Qualifiers
     source          1. .1081
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                     /db_xref="GI:307164"
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                     ISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAV
                     DTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN"
ORIGIN       Unreported.

  Query Match             90.2%;  Score 1080;  DB 9;  Length 1081;
  Best Local Similarity   100.0%;  Pred. No. 8.8e-239;
  Matches 1080;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         74 CAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACT 133
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Qy        134 CTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAA 193
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Db         62 CTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAA 121

Qy        194 CCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTT 253
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Db        122 CCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTT 181

Qy        254 ACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGC 313
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Db        182 ACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGC 241

Qy        314 CTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGA 373
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Db        542 GACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCC 601

Qy        674 CTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCA 733
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Qy        974 AACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTAAGT 1033
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Db        902 AACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTAAGT 961

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RESULT 11
BC015195
LOCUS       BC015195                1106 bp    mRNA    linear   PRI 06-OCT-2003
DEFINITION  Homo sapiens Fc fragment of IgE, high affinity I, receptor for;
            alpha polypeptide, mRNA (cDNA clone MGC:14717 IMAGE:4251469),
            complete cds.
ACCESSION   BC015195
VERSION     BC015195.1  GI:15929529
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1106)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
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            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
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            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1106)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-OCT-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
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          R. M.

          Clone distribution: MGC clone distribution information can be found
          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
          Series: IRAL Plate: 21 Row: a Column: 14
          This clone was selected for full length sequencing because it
          passed the following selection criteria: Similarity but not
          identity to protein.
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                     /note="Vector: pDNR-LIB"
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                     /db_xref="LocusID:2205"
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                     ISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAV
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  Matches 1089;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          75 AGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTC 134
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Db           2 AGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTC 61

Qy         135 TACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAAC 194
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Qy         195 CTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTA 254
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Qy         255 CATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCC 314
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Qy         315 TTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAG 374
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Qy         375 AATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCA 434
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Qy         615 ACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCC 674
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Qy         675 TCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCAT 734
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Qy         735 TGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGG 794
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Qy         795 TCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATC 854
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Db         722 CCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATC 781

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Db         782 CTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATATTTGCAACATTAGTT 841

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Qy        1155 ACAGAATGCTTCTGAGTAAAAAAAA 1179
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RESULT 12
BC005912
LOCUS       BC005912                1102 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens Fc fragment of IgE, high affinity I, receptor for;
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            complete cds.
ACCESSION   BC005912
VERSION     BC005912.1  GI:13543505
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1102)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
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            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
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  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1102)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-APR-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 21 Row: h Column: 16
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4503674.
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                     /note="Vector: pDNR-LIB"
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                     /db_xref="MIM:147140"
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ORIGIN

  Query Match             90.0%;  Score 1078;  DB 9;  Length 1102;
  Best Local Similarity   98.6%;  Pred. No. 2.6e-238;
  Matches 1087;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         78 ACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTAC 137
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTAC 60

Qy        138 TGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTA 197
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTA 120

Qy        198 AGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTACAT 257
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTACAT 180

Qy        258 GTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTT 317
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTT 240

Qy        318 CAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAAT 377
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAAT 300

Qy        378 ACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTG 437
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTG 360

Qy        438 ACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCA 497
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCA 420

Qy        498 GGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAG 557
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAG 480

Qy        558 CTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACA 617
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACA 540

Qy        618 GTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCA 677
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCA 600

Qy        678 ACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGT 737
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGT 660

Qy        738 TGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCA 797
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCA 720

Qy        798 CATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTA 857
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTA 780

Qy        858 AGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTT 917
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTT 840

Qy        918 TTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATATACATAGAAACG 977
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATATACATAGAAACG 900

Qy        978 TCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTAAGTGGCA 1037
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTAAGTGGCA 960

Qy       1038 TGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAATGAATAGATTCATT 1097
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 TGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAATGAATAGATTCATT 1020
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Qy       1098 TATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAATATAAAACCATGTAACA 1157
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  || |
Db       1021 TATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAATATAAAACCAAAAAAAA 1080

Qy       1158 GAATGCTTCTGAGTAAAAAAAA 1179
              ||         | ||||||||
Db       1081 AAAAAAAAAAAAAAAAAAAAA 1102


RESULT 13
A21606
LOCUS       A21606                 1068 bp    DNA     linear   PAT 21-JUL-1994
DEFINITION  human FC epsilon RIIa.
ACCESSION   A21606
VERSION     A21606.1  GI:579605
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1068)
  AUTHORS   .
  TITLE     HYBRID Fc RECEPTOR MOLECULES
  JOURNAL   Patent: WO 9106570-A 29 16-MAY-1991;
FEATURES             Location/Qualifiers
     source          1. .1068
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
     gene            40. .813
                     /gene="FC epsilon RIIa"
     CDS             40. .813
                     /gene="FC epsilon RIIa"
                     /codon_start=1
                     /protein_id="CAA01564.1"
                     /db_xref="GI:579606"
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                     /db_xref="SWISS-PROT:P12319"
                     /translation="MAPAMESPTLLCVALLFPAPDGVLAVPQKPKVSLNPPWNRIFKG
                     ENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESE
                     PVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHN
                     ISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAV
                     DTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN"
ORIGIN

  Query Match             87.1%;  Score 1043.2;  DB 6;  Length 1068;
  Best Local Similarity   99.6%;  Pred. No. 2.8e-230;
  Matches 1056;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy         74 CAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACT 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 CAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACT 66

Qy        134 CTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAA 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAA 126

Qy        194 CCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTT 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTT 186

Qy        254 ACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGC 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGC 246

Qy        314 CTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGA 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGA 306

Qy        374 GAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTC 433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTC 366

Qy        434 AGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTC 493
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Db        367 AGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTC 426

Qy        494 CTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGT 553
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 CTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGT 486

Qy        554 GAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAA 613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 GAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAA 546

Qy        614 GACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCC 673
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCC 606

Qy        674 CTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCA 733
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 CTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCA 666

Qy        734 TTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAG 793
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Db        667 TTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAG 726

Qy        794 GTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACAT 853
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Db        727 GTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACAT 786

Qy        854 CCTAAGCCAAACCCCAAAAACAACTGATATAATT-ACTCAAGAAATATTTGCAACATTAG 912
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db        787 CCTAAGCCAAACCCCAAAAACAACTGATATAATTAACTCAAGAAATATTTGCAACATTAG 846

Qy        913 TTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATATACATAG 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATATACATAG 906

Qy        973 AAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTAAG 1032
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Db        907 AAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGATTAAG 966

Qy       1033 TGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAATGAATAGAT 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAATGAATAGAT 1026

Qy       1093 TCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAAT 1132
              |||||||||||||||||||||||||||||||||||||  ||
Db       1027 TCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTAGAT 1066


RESULT 14
BD264325
LOCUS       BD264325               1068 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Recombinant soluble Fc receptors.
ACCESSION   BD264325
VERSION     BD264325.1  GI:33074093
KEYWORDS    JP 2002531086-A/8.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1068)
  AUTHORS   Sondermann,P., Huber,R. and Jakob,U.
  TITLE     Recombinant soluble Fc receptors
  JOURNAL   Patent: JP 2002531086-A 8 24-SEP-2002;
            MAX PLANCK GESELLSCHAFT ZUR FOERDERUNG DER WISSENSCHAFTEN EV
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002531086-A/8
            PD   24-SEP-2002
            PF   03-DEC-1999 JP 2000585398
            PR   03-DEC-1998 EP   98122969.3
            PI   PETER SONDERMANN,ROBERT HUBER,UWE JAKOB
            PC   C12N15/09,A61K38/00,A61K45/00,A61P19/02,A61P29/00,A61P31/18,
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PC   A61P35/00,
PC   A61P37/02,A61P37/08,C07K14/735,C12N1/21,G01N33/53,G01N33/53//
PC   (C12N1/21,C12R1:19),C12N15/00,A61K37/02
CC   Description of Artificial Sequence: Primer
FH   Key             Location/Qualifiers
FT   source          1. .1068
FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .1068
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                     /db_xref="taxon:9606"
ORIGIN

  Query Match            87.1%;  Score 1043.2;  DB 6;  Length 1068;
  Best Local Similarity  99.6%;  Pred. No. 2.8e-230;
  Matches 1056;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy         74 CAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACT 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          7 CAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACT 66

Qy        134 CTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAA 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAA 126

Qy        194 CCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTT 253
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Db        127 CCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTT 186

Qy        254 ACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGC 313
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Db        187 ACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGC 246

Qy        314 CTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGA 373
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Db        247 CTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGA 306

Qy        374 GAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTC 433
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Db        307 GAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTC 366

Qy        434 AGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTC 493
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Db        367 AGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTC 426

Qy        494 CTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGT 553
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Db        427 CTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGT 486

Qy        554 GAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAA 613
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Db        487 GAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAA 546

Qy        614 GACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCC 673
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Qy        674 CTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCA 733
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Db        607 CTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCA 666

Qy        734 TTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAG 793
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Db        667 TTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAG 726

Qy        794 GTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACAT 853
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 GTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACAT 786

Qy        854 CCTAAGCCAAACCCCAAAAACAACTGATATAATT-ACTCAAGAAATATTTGCAACATTAG 912
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        787 CCTAAGCCAAACCCCAAAAACAACTGATATAATTAACTCAAGAAATATTTGCAACATTAG 846

Qy        913 TTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATATACATAG 972
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Db        847 TTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATATACATAG 906

Qy        973 AAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTAAG 1032
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Db        907 AAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGATTAAG 966

Qy       1033 TGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAATGAATAGAT 1092
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Db        967 TGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAATGAATAGAT 1026

Qy       1093 TCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAAT 1132
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Db       1027 TCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTAGAT 1066


RESULT 15
AX026808
LOCUS       AX026808               1068 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 14 from Patent EP1006183.
ACCESSION   AX026808
VERSION     AX026808.1  GI:10187941
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   .
  TITLE     Recombinant soluble fc receptors
  JOURNAL   Patent: EP 1006183-A 14 07-JUN-2000;
            MAX PLANCK GESELLSCHAFT (DE)
FEATURES             Location/Qualifiers
     source          1. .1068
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
ORIGIN

  Query Match            87.1%;  Score 1043.2;  DB 6;  Length 1068;
  Best Local Similarity  99.6%;  Pred. No. 2.8e-230;
  Matches 1056;  Conservative    0;  Mismatches    3;  Indels    1;  Gaps    1;

Qy         74 CAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACT 133
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Db          7 CAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACT 66

Qy        134 CTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAA 193
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 CTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAA 126

Qy        194 CCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTT 253
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTT 186

Qy        254 ACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGC 313
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGC 246

Qy        314 CTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGA 373
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 CTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGA 306

Qy        374 GAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTC 433
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        307 GAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTC 366

Qy        434 AGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTC 493
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        494 CTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGT 553
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Db        427 CTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGT 486

Qy        554 GAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAA 613
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        487 GAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAA 546

Qy        614 GACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCC 673
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 GACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCC 606

Qy        674 CTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCA 733
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 CTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCA 666

Qy        734 TTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAG 793
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        667 TTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAG 726

Qy        794 GTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACAT 853
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        727 GTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACAT 786

Qy        854 CCTAAGCCAAACCCCAAAAACAACTGATATAATT-ACTCAAGAAATATTTGCAACATTAG 912
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        787 CCTAAGCCAAACCCCAAAAACAACTGATATAATTAACTCAAGAAATATTTGCAACATTAG 846

Qy        913 TTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATATACATAG 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        847 TTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATATACATAG 906

Qy        973 AAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTAAG 1032
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        907 AAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGATTAAG 966

Qy       1033 TGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAATGAATAGAT 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        967 TGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAATGAATAGAT 1026

Qy       1093 TCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAAT 1132
              |||||||||||||||||||||||||||||||||||  ||
Db       1027 TCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTAGAT 1066
```

Search completed: October 10, 2004, 16:11:54
Job time : 5220.6 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 8, 2004, 15:03:47 ; Search time 582.511 Seconds
(without alignments)
8736.904 Million cell updates/sec

Title: US-10-763-400-1
Perfect score: 1198
Sequence: 1 tactaagagtctccagcatc.....aaaaaaaaaaaaaaaaaaa 1198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1198	100.0	1198	2	AAV36343	Aav36343 cDNA enco
	2	1198	100.0	1198	3	AAA34813	Aaa34813 Human ade
	3	1198	100.0	1198	3	AAF20935	Aaf20935 Human hig
	4	1198	100.0	1198	4	AAF77692	Aaf77692 Human wil
c	5	1198	100.0	1198	5	AAF24912	Aaf24912 Complemen
	6	1198	100.0	1198	5	AAF24911	Aaf24911 Nucleotid
	7	1198	100.0	1198	6	ABL67793	Abl67793 Oesophagu
	8	1198	100.0	1198	7	ABZ96629	Abz96629 Human hig
	9	1198	100.0	1198	9	ADB85535	Adb85535 Human imm
	10	1198	100.0	21742	3	AAA34816	Aaa34816 Human ade
	11	1198	100.0	21742	3	AAF20938	Aaf20938 Human hig
	12	1198	100.0	21742	7	ABZ96632	Abz96632 Human hig
	13	1198	100.0	117608	7	ABZ97129	Abz97129 Human rec
	14	1198	100.0	117609	3	AAF21435	Aaf21435 Human rec
	15	1190	99.3	1199	2	AAQ14736	Aaq14736 Human Fc(
	16	1186	99.0	1197	2	AAT85615	Aat85615 Alpha sub
	17	1183.4	98.8	1193	2	AAQ04644	Aaq04644 Encodes a
	18	1144.8	95.6	1174	2	AAQ51020	Aaq51020 Human Fce
	19	1083.8	90.5	1088	1	AAN90126	Aan90126 cDNA enco
	20	1043.2	87.1	1068	3	AAA27470	Aaa27470 Human Fc
	21	922.2	77.0	1150	2	AAQ34840	Aaq34840 Human hig
	22	882.8	73.7	898	8	ACD06182	Acd06182 Human cDN
	23	774	64.6	774	4	AAF97964	Aaf97964 Human imm
	24	773	64.5	773	6	ABS52959	Abs52959 Human cDN
	25	771.4	64.4	773	2	AAV20402	Aav20402 Human IgE
	26	705.4	58.9	851	2	AAQ27267	Aaq27267 Human FcE
	27	697	58.2	713	2	AAQ55969	Aaq55969 Human dih
c	28	696	58.1	696	5	AAF24914	Aaf24914 Complemen
	29	696	58.1	696	5	AAF24913	Aaf24913 Nucleotid
	30	630	52.6	757	8	ACD06183	Acd06183 Human cDN
	31	611	51.0	2955	2	AAV20404	Aav20404 Plasmid R
	32	611	51.0	2955	6	ABS52957	Abs52957 Human cDN
c	33	591	49.3	591	5	AAF24916	Aaf24916 Complemen
	34	591	49.3	591	5	AAF24915	Aaf24915 DNA encod
c	35	591	49.3	1983	5	AAF24927	Aaf24927 Fc epsilo
	36	591	49.3	1983	5	AAF24926	Aaf24926 Fc epsilo
c	37	591	49.3	2268	5	AAF24921	Aaf24921 Complemen
	38	591	49.3	2268	5	AAF24920	Aaf24920 Nucleotid
	39	578.8	48.3	1015	2	AAX89856	Aax89856 Equine Fc
c	40	578.8	48.3	1015	2	AAX89857	Aax89857 Equine Fc
	41	554	46.2	570	3	AAA27472	Aaa27472 Recombina
	42	528	44.1	528	3	AAA27301	Aaa27301 Human Fce
	43	528	44.1	528	4	AAH47768	Aah47768 Nucleotid
	44	516	43.1	516	3	AAA27302	Aaa27302 Human nhF
	45	516	43.1	516	5	AAF24917	Aaf24917 DNA encod

ALIGNMENTS

RESULT 1
AAV36343
ID AAV36343 standard; cDNA; 1198 BP.
XX
AC AAV36343;
XX
DT 07-OCT-1998 (first entry)
XX
DE cDNA encoding the alpha chain of a Fc epsilon receptor.
XX
KW Alpha chain; human; Fc epsilon receptor; canine; equine; feline;
KW immunoglobulin E; IgE; detection; diagnose; allergy; atopic disease;
KW hyper-IgE syndrome; internal parasitic infection; B cell neoplasia;
KW flea allergy; heartworm infection; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 107. .880
FT /*tag= a
XX
PN WO9823964-A1.
XX
PD 04-JUN-1998.
XX
PF 24-NOV-1997; 97WO-US021651.
XX
PR 26-NOV-1996; 96US-00756387.
XX
PA (HESK-) HESKA CORP.
XX
PI Frank RG, Porter JP, Rushlow KE, Wassom DL;
XX
DR WPI; 1998-322873/28.
DR P-PSDB; AAW61190.
XX
PT Detection of non-human immunoglobulin E - by complex formation with human
PT Fc epsilon receptor, used for, e.g. diagnosis of allergy and atopic
PT disease.
XX
PS Claim 11; Page 36-37; 70pp; English.
XX
CC The present sequence encodes the alpha chain of the human Fc epsilon
CC receptor. Detection of canine, equine or feline immunoglobulin E (IgE)
CC comprises reacting isolated human Fc epsilon receptor with the test
CC sample and detecting formation of a IgE-receptor complex. Detection of

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CC   IgE is used to diagnose allergy, atopic disease, hyper-IgE syndrome,
CC   internal parasitic infections or B cell neoplasia, and for measuring
CC   effect of treatments. Most particularly flea allergy in dogs and cats is
CC   detected, and also heartworm infection
XX
SQ   Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 1198;  DB 2;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-230;
  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198


RESULT 2
AAA34813
ID   AAA34813 standard; DNA; 1198 BP.
XX
AC   AAA34813;
XX
DT   28-JUL-2000  (first entry)
XX
DE   Human adenosine receptor related polynucleotide SEQ ID NO:2502.
XX
KW   Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW   phosphorothioate; impaired respiration; inflammation; allergy;
KW   allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW   antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW   lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW   respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW   pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW   cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS   Homo sapiens.
XX
PN   WO200009525-A2.
XX
PD   24-FEB-2000.
XX
PF   03-AUG-1999;   99WO-US017712.
XX
PR   03-AUG-1998;   98US-0095212P.
XX
PA   (UYEC-) UNIV EAST CAROLINA.
XX
PI   Nyce JW;
XX
DR   WPI; 2000-205971/18.
XX
PT   New antisense oligonucleotides useful for treating e.g. pulmonary
PT   vasoconstruction, inflammation, allergies, asthma, hypertension,
PT   bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT   cancers.
XX
PS   Disclosure; Page 655; 1343pp; English.
XX
CC   The present invention describes a new composition comprising an antisense
CC   oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC   nucleic acids involved in bronchoconstriction, allergies, and/or
CC   inflammation. The ON can have antiinflammatory, antiallergic,
CC   antiasthmatic, cytostatic and analgesic activities. The compositions are
CC   useful for the treatment of diseases associated with inflammation,
CC   impaired airways, including lung disease and diseases whose secondary
CC   effects afflict the lungs of a subject. They can be used for treating
CC   e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC   impeded respiration, respiratory distress syndrome, pain, cystic
CC   fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC   pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
```

CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 1198; DB 3; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2.3e-230;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
```

RESULT 3
AAF20935
ID AAF20935 standard; DNA; 1198 BP.
XX
AC AAF20935;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human high affinity IgE receptor polynucleotide fragment #2502.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Disclosure; Page 138; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense

```
CC   oligonucleotides and compositions (I) comprising them. In the antisense
CC   oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC   (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC   immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC   The antisense oligonucleotides and (I) can be used to down-regulate the
CC   expression and or activity of target polypeptides associated with
CC   lung/respiratory disorders and malignancies, such as stimulating and
CC   activating peptide factors and transmitters, transcription factors,
CC   immunoglobulins and antibodies, antibody receptors, cytokines and
CC   chemokines, endogenously produced specific and non-specific enzymes,
CC   binding proteins, adhesion molecules and their receptors, cytokine and
CC   chemokine receptors, adenosine receptors, bradykinin receptors, central
CC   nervous system (CNS) and peripheral nervous and non-nervous system
CC   receptors, CNS and peripheral nervous and non-nervous system peptide
CC   transmitters, defensins, growth factors, vasoactive peptides and
CC   receptors, binding proteins and malignancy associated proteins. The
CC   antisense oligonucleotides may be used in this way to treat disorders
CC   including respiratory obstruction (especially pulmonary obstruction
CC   and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC   surfactant hypoproduction which are associated with a disease or
CC   condition selected from pulmonary vasoconstriction, inflammation,
CC   allergies, asthma, impeded respiration, respiratory distress syndrome
CC   (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC   pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC   and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC   fragments and antisense oligonucleotides used in the exemplification of
CC   the present invention
XX
SQ   Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1198;  DB 3;  Length 1198;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-230;
  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAA 1198


RESULT 4
AAF77692
ID   AAF77692 standard; cDNA; 1198 BP.
XX
AC   AAF77692;
XX
DT   29-MAY-2001  (first entry)
XX
DE   Human wild-type FcepsilonRIalpha chain coding sequence.
XX
KW   Human; FcepsilonRIbeta chain; immunoglobulin E; allergy; atopy;
KW   conjunctivitis; rhinitis; anaphylaxis; urticaria; angioedema; ss.
XX
OS   Homo sapiens.
XX
PN   WO200121816-A1.
XX
PD   29-MAR-2001.
XX
PF   21-SEP-2000; 2000WO-US025877.
XX
PR   21-SEP-1999;   99US-0154924P.
XX
PA   (ISIS-) ISIS INNOVATION LTD.
PA   (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI   Kinet J,  Donnadieu E,  Jouvin M,  Cookson W,  Moffatt MF;
XX
DR   WPI; 2001-266077/27.
XX
```

PT Inhibiting expression of high affinity receptors for immunoglobulin (Ig)
PT E, in cell or in subject to treat atopy, anaphylaxis mediated by IgE, by
PT contacting cell or administering to subject, a FcERIbeta chain variant.
XX
PS Disclosure; Page 52; 55pp; English.
XX
CC The present invention describes a method of inhibiting the expression of
CC the FcepsilonRI receptor by contacting a cell expressing it with an
CC FcepsilonRIbeta chain variant. The Fcepsilon receptor is a high affinity
CC receptor for immunoglobulin E. The method is useful in the treatment of
CC allergic conditions such as rhinitis, conjunctivitis, atopy, anaphylaxis,
CC urticaria and angioedema. The present sequence is the wild-type human
CC FcepsilonRIalpha chain coding sequence
XX
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 1198; DB 4; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2.3e-230;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
```

RESULT 5
AAF24912/c
ID AAF24912 standard; DNA; 1198 BP.
XX
AC AAF24912;
XX
DT 30-APR-2001 (first entry)
XX
DE Complement sequence of a human Fc epsilon receptor alpha-chain gene.
XX
KW Fc epsilon receptor; FcepsilonR; immunoglobulin E; IgE; atopic disease;
KW luminescence inducing protein; allergy; hyper IgE syndrome;
KW internal parasite infection; B cell neoplasia; ss.
XX
OS Homo sapiens.
XX
PN WO200104310-A1.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US019070.
XX
PR 13-JUL-1999; 99US-0143612P.
PR 02-MAR-2000; 2000US-0186412P.
XX
PA (HESK-) HESKA CORP.
PA (PROM-) PROMEGA CORP.
XX
PI Weber ER, Wood KV, Hall MP;
XX
DR WPI; 2001-103082/11.
XX
PT A fusion protein, comprising an Fc epsilon receptor domain and a
PT luminescence inducing protein domain that induces a LP substrate to emit
PT light when contacted with the LP domain, useful for detecting
PT immunoglobulin (Ig) E.
XX
PS Example; Page 61; 105pp; English.
XX
CC The present sequence represents the complement of a human Fc epsilon
CC receptor (FcepsilonR) alpha-chain protein, that binds to immunoglobulin
CC (Ig) E). The FcepsilonR domain is used to produce a fusion protein, which
CC also comprises a luminescence inducing protein domain that induces a
CC substrate to emit light when contacted with the luminescence inducing
CC protein domain. The fusion protein may be used to detect IgE. It may also

```
CC   be used to identify a compound capable of inhibiting FcepsilonR protein
CC   activity. IgE antibody production is indicative of diseases such as
CC   allergies, atopic disease, hyper IgE syndrome, internal parasite
CC   infections and B cell neoplasia. Detection of IgE production in an animal
CC   following therapy is indicative of the efficacy of the treatment, for
CC   example when using treatments intended to disrupt IgE production
XX
SQ   Sequence 1198 BP; 321 A; 245 C; 243 G; 389 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 1198;  DB 5;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-230;
  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 1139

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 1079

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 1019

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 959

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 899

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 839

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 779

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 719

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 659

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 599

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 539

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 479

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 419

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 359

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 299

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 239

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 179

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 119

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 59

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          58 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 6
AAF24911
ID   AAF24911 standard; DNA; 1198 BP.
XX
AC   AAF24911;
XX
DT   30-APR-2001  (first entry)
XX
DE   Nucleotide sequence of a human Fc epsilon receptor alpha-chain.
XX
KW   Fc epsilon receptor; FcepsilonR; immunoglobulin E; IgE; atopic disease;
KW   luminescence inducing protein; allergy; hyper IgE syndrome;
KW   internal parasite infection; B cell neoplasia; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             107. .880
FT                   /*tag= a
FT                   /product= "Fc epsilon receptor alpha-chain"
XX
PN   WO200104310-A1.
XX
PD   18-JAN-2001.
XX
PF   13-JUL-2000; 2000WO-US019070.
XX
PR   13-JUL-1999;   99US-0143612P.
PR   02-MAR-2000; 2000US-0186412P.
XX
PA   (HESK-) HESKA CORP.
PA   (PROM-) PROMEGA CORP.
XX
PI   Weber ER,  Wood KV,  Hall MP;
XX
DR   WPI; 2001-103082/11.
DR   P-PSDB; AAB31584.
XX
PT   A fusion protein, comprising an Fc epsilon receptor domain and a
PT   luminescence inducing protein domain that induces a LP substrate to emit
PT   light when contacted with the LP domain, useful for detecting
PT   immunoglobulin (Ig) E.
XX
PS   Claim 17; Page 58-59; 105pp; English.
XX
CC   The present sequence encodes a human Fc epsilon receptor (FcepsilonR)
CC   alpha-chain protein, that binds to immunoglobulin (Ig) E). The FcepsilonR
CC   domain is used to produce a fusion protein, which also comprises a
CC   luminescence inducing protein domain that induces a substrate to emit
CC   light when contacted with the luminescence inducing protein domain. The
CC   fusion protein may be used to detect IgE. It may also be used to identify
CC   a compound capable of inhibiting FcepsilonR protein activity. IgE
```

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CC   antibody production is indicative of diseases such as allergies, atopic
CC   disease, hyper IgE syndrome, internal parasite infections and B cell
CC   neoplasia. Detection of IgE production in an animal following therapy is
CC   indicative of the efficacy of the treatment, for example when using
CC   treatments intended to disrupt IgE production
XX
SQ   Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

  Query Match            100.0%;  Score 1198;  DB 5;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-230;
  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
```

```
RESULT 7
ABL67793
ID   ABL67793 standard; DNA; 1198 BP.
XX
AC   ABL67793;
XX
DT   15-MAY-2002  (first entry)
XX
DE   Oesophagus cancer related gene sequence SEQ ID NO:6130.
XX
KW   Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW   stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW   cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW   gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO200194629-A2.
XX
PD   13-DEC-2001.
XX
PF   30-MAY-2001; 2001WO-US010838.
XX
PR   05-JUN-2000; 2000US-0209473P.
PR   05-JUN-2000; 2000US-0209531P.
PR   18-SEP-2000; 2000US-0233133P.
PR   18-SEP-2000; 2000US-0233617P.
PR   20-SEP-2000; 2000US-0234009P.
PR   20-SEP-2000; 2000US-0234034P.
PR   20-SEP-2000; 2000US-0234052P.
PR   22-SEP-2000; 2000US-0234509P.
PR   22-SEP-2000; 2000US-0234567P.
PR   25-SEP-2000; 2000US-0234923P.
PR   25-SEP-2000; 2000US-0234924P.
PR   25-SEP-2000; 2000US-0235077P.
PR   25-SEP-2000; 2000US-0235082P.
PR   25-SEP-2000; 2000US-0235134P.
PR   25-SEP-2000; 2000US-0235280P.
PR   26-SEP-2000; 2000US-0235637P.
PR   26-SEP-2000; 2000US-0235638P.
PR   27-SEP-2000; 2000US-0235711P.
PR   27-SEP-2000; 2000US-0235720P.
PR   27-SEP-2000; 2000US-0235840P.
PR   27-SEP-2000; 2000US-0235863P.
PR   28-SEP-2000; 2000US-0236028P.
PR   28-SEP-2000; 2000US-0236032P.
PR   28-SEP-2000; 2000US-0236033P.
PR   28-SEP-2000; 2000US-0236034P.
PR   28-SEP-2000; 2000US-0236109P.
PR   28-SEP-2000; 2000US-0236111P.
PR   29-SEP-2000; 2000US-0236842P.
PR   29-SEP-2000; 2000US-0236891P.
PR   02-OCT-2000; 2000US-0237172P.
```

PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 6130; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC tumour
XX
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 1198; DB 6; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2.3e-230;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
```

RESULT 8
ABZ96629
ID ABZ96629 standard; DNA; 1198 BP.
XX
AC ABZ96629;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human high affinity IgE receptor oligonucleotide fragment.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;

KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 11871; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 1198; DB 7; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2.3e-230;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
```

RESULT 9
ADB85535
ID ADB85535 standard; cDNA; 1198 BP.
XX
AC ADB85535;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human immunoglobulin E high affinity receptor (FcERI) alpha subunit cDNA.
XX
KW alpha subunit; high affinity receptor for immunoglobulin E; FcERI;
KW mast cell; basophil; histamine; serotonin; allergic condition;

```
KW   antiallergic; allergic response; drug screening assay; immunoglobulin E;
KW   human; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             107. .880
FT                   /*tag=  a
FT                   /product= "Human FcERI receptor"
FT                   /transl_except= (767. .769, aa:Glu)
FT                   /transl_except= (863. .865, aa:Asp)
XX
PN   US6602983-B1.
XX
PD   05-AUG-2003.
XX
PF   22-SEP-1994;   94US-00310902.
XX
PR   24-FEB-1988;   88US-00160457.
PR   30-OCT-1991;   91US-00785127.
PR   29-MAY-1993;   93US-00066640.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Kinet JP,  Kochan JP;
XX
DR   WPI; 2003-669612/63.
DR   P-PSDB; ADB85536.
XX
PT   New alpha subunit of the human high affinity receptor for immunoglobulin
PT   E polypeptides, useful as antagonists to prevent allergic response, as
PT   reagents in drug screening assays, or for monitoring immunoglobulin E
PT   levels in patients.
XX
PS   Claim 1; Fig 1; 9pp; English.
XX
CC   This invention relates to a novel purified polypeptide corresponding to
CC   the alpha subunit of the human high affinity receptor for immunoglobulin
CC   E (FcERI) and the DNA sequence which encodes it. The receptor of the
CC   invention is found exclusively on mast cells, basophils and related
CC   cells. Activation of the receptor triggers the release of preformed
CC   mediators such as histamine and serotonin which may result in allergic
CC   conditions. Compounds which modulate FcERI activity may have antiallergic
CC   activity. The polypeptide of the invention may be useful as an antagonist
CC   for preventing allergic response, as a reagent in drug screening assays,
CC   as a therapeutic or for monitoring immunoglobulin E levels in patients.
CC   The DNA sequences may be useful for producing the polypeptide or for
CC   synthesising cDNA sequences to construct DNA probes used in diagnostic
CC   assays. The present sequence is the cDNA sequence encoding the alpha
CC   subunit of the human FcERI receptor of the invention.
XX
SQ   Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 1198;  DB 9;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-230;
  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198


RESULT 10
AAA34816
ID   AAA34816 standard; DNA; 21742 BP.
XX
AC   AAA34816;
XX
DT   28-JUL-2000  (first entry)
XX
```

DE Human adenosine receptor related polynucleotide SEQ ID NO:2505.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstruction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 658-664; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 21742 BP; 6598 A; 4107 C; 4408 G; 6612 T; 0 U; 17 Other;

Query Match 100.0%; Score 1198; DB 3; Length 21742;
Best Local Similarity 100.0%; Pred. No. 3.8e-230;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8353 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 8412

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8413 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 8472

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8473 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 8532

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8533 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 8592

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8593 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 8652

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8653 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 8712

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8713 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 8772

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8773 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 8832

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8833 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 8892

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8893 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 8952

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8953 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 9012

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9013 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 9072

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9073 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 9132

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9133 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 9192

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9193 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 9252

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9253 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 9312

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9313 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 9372

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9373 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 9432

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9433 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 9492

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9493 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9550
```

RESULT 11
AAF20938
ID AAF20938 standard; DNA; 21742 BP.
XX
AC AAF20938;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human high affinity IgE receptor polynucleotide fragment #2505.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Disclosure; Page 131-136; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 21742 BP; 6598 A; 4107 C; 4408 G; 6612 T; 0 U; 17 Other;

Query Match 100.0%; Score 1198; DB 3; Length 21742;
Best Local Similarity 100.0%; Pred. No. 3.8e-230;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8353 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 8412

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8413 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 8472

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8473 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 8532

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8533 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 8592

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8593 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 8652

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8653 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 8712

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8713 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 8772

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8773 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 8832

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8833 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 8892

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8893 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 8952

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8953 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 9012

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9013 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 9072

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9073 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 9132

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9133 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 9192

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9193 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 9252

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9253 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 9312

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9313 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 9372

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9373 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 9432

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9433 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 9492

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9493 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAA 9550
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RESULT 12
ABZ96632
ID ABZ96632 standard; DNA; 21742 BP.
XX
AC ABZ96632;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human high affinity IgE receptor oligonucleotide fragment.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 11874; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 21742 BP; 6598 A; 4107 C; 4408 G; 6612 T; 0 U; 17 Other;

Query Match 100.0%; Score 1198; DB 7; Length 21742;
Best Local Similarity 100.0%; Pred. No. 3.8e-230;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8353 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 8412

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8413 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 8472

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8473 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 8532

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8533 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 8592

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8593 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 8652

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8653 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 8712

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8713 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 8772

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8773 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 8832

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8833 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 8892

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8893 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 8952

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8953 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 9012

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9013 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 9072

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9073 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 9132

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9133 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 9192

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9193 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 9252

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       9253 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 9312

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9313 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 9372

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9373 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 9432

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9433 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 9492

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9493 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 9550
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RESULT 13
ABZ97129
ID ABZ97129 standard; DNA; 117608 BP.
XX
AC ABZ97129;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human receptor-related antisense polynucleotide.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 12371; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 117608 BP; 27528 A; 29941 C; 30321 G; 29442 T; 0 U; 376 Other;

Query Match 100.0%; Score 1198; DB 7; Length 117608;
Best Local Similarity 100.0%; Pred. No. 5e-230;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100755 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 100814

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
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Db     100815 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 100874

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100875 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 100934

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100935 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 100994

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100995 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 101054

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101055 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 101114

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101115 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 101174

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101175 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 101234

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101235 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 101294

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101295 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 101354

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101355 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 101414

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101415 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 101474

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101475 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 101534

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101535 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 101594

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
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Db     101595 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 101654
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Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
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Db     101655 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 101714

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
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Db     101715 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 101774

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
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Db     101775 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 101834

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101835 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 101894

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101895 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 101952
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RESULT 14
AAF21435
ID AAF21435 standard; DNA; 117609 BP.
XX
AC AAF21435;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human receptor-related antisense polynucleotide #3002.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Disclosure; Page 17-47; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 117609 BP; 27530 A; 29942 C; 30320 G; 29441 T; 0 U; 376 Other;

Query Match 100.0%; Score 1198; DB 3; Length 117609;
Best Local Similarity 100.0%; Pred. No. 5e-230;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100756 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 100815

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100816 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 100875

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100876 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 100935

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100936 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 100995

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     100996 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 101055

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101056 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 101115

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101116 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 101175

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101176 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 101235

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101236 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 101295

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101296 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 101355

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101356 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 101415
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Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101416 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 101475

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101476 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 101535

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101536 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 101595

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101596 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 101655

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
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Db     101656 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 101715

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101716 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 101775

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101776 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 101835

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101836 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 101895

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     101896 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 101953
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RESULT 15
AAQ14736
ID   AAQ14736 standard; cDNA; 1199 BP.
XX
AC   AAQ14736;
XX
DT   25-MAR-2003  (revised)
DT   17-DEC-2001  (revised)
DT   03-FEB-1992  (first entry)
XX
DE   Human Fc(epsilon)RI alpha cDNA.
XX
KW   Immunoglobulin; receptor; high affinity receptor; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             107. .880
FT                   /*tag= a
FT                   /product= "alpha_subunit"
XX
PN   USN7626704-N.
XX
PD   15-OCT-1991.
XX
PF   14-DEC-1990;   90US-00626704.
XX
PR   14-DEC-1990;   90US-00626704.
XX
PA   (USSH ) NAT INST OF HEALTH.
XX
PI   Kinet JP,  Metzger H;
XX
DR   WPI; 1991-346755/47.
DR   P-PSDB; AAR14772.
XX
PT   DNA coding alpha, beta and gamma-units of ige high affinity receptor -
PT   are used to prepare recombinant polypeptide(s) for treating allergy, drug
PT   screening or monitoring IgE level.
XX
PS   Disclosure; Fig 1; 58pp; English.
XX
CC   A lambda gt11 library was prepared from poly-A RNA isolated from KUB12
CC   cells. Screening was by a cDNA fragment from the rat Fc(epsilon)RI alpha
CC   cDNA corresponding to nucleotides 119-781. Positive clones were subcloned
CC   and sequenced. (Note: Revised entry submitted to correct the patent
CC   number format of US Government-owned NTIS applications to prevent clashes
CC   with ongoing US granted patent numbers. For further information please
CC   visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.)
CC   (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 1199 BP; 390 A; 241 C; 247 G; 321 T; 0 U; 0 Other;
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  Query Match             99.3%;  Score 1190;  DB 2;  Length 1199;
  Best Local Similarity   99.6%;  Pred. No. 9.4e-229;
  Matches 1193;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
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Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
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Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
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Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
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Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
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Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
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Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
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Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
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Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
```

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Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTGACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
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Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
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Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
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Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              |||||||||||||||||||||||||   |||||||||||||||||||||||||
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Search completed: October 8, 2004, 23:17:37
Job time : 585.511 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:14:29 ; Search time 105.911 Seconds
(without alignments)
6277.259 Million cell updates/sec

Title: US-10-763-400-1
Perfect score: 1198
Sequence: 1 tactaagagtctccagcatc.....aaaaaaaaaaaaaaaaaaa 1198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1198	100.0	1198	2	US-08-756-387B-1	Sequence 1, Appli
c	2	1198	100.0	1198	2	US-08-756-387B-3	Sequence 3, Appli
	3	1198	100.0	1198	4	US-09-285-873-1	Sequence 1, Appli
c	4	1198	100.0	1198	4	US-09-285-873-3	Sequence 3, Appli
	5	1198	100.0	1198	4	US-09-944-277A-1	Sequence 1, Appli
c	6	1198	100.0	1198	4	US-09-944-277A-3	Sequence 3, Appli
	7	1144.8	95.6	1174	1	US-07-869-933-10	Sequence 10, Appl
	8	1144.8	95.6	1174	3	US-09-103-663-10	Sequence 10, Appl
	9	774	64.6	774	2	US-08-756-387B-4	Sequence 4, Appli
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	15	773	64.5	773	4	US-08-897-956A-6	Sequence 6, Appli
	16	699	58.3	699	2	US-08-756-387B-7	Sequence 7, Appli
	17	699	58.3	699	4	US-09-285-873-7	Sequence 7, Appli
	18	699	58.3	699	4	US-09-944-277A-7	Sequence 7, Appli
	19	697	58.2	713	2	US-08-238-027-3	Sequence 3, Appli
	20	611	51.0	2955	4	US-08-897-956A-4	Sequence 4, Appli
	21	591	49.3	591	2	US-08-756-387B-10	Sequence 10, Appl
	22	591	49.3	591	4	US-09-285-873-10	Sequence 10, Appl
	23	591	49.3	591	4	US-09-944-277A-10	Sequence 10, Appl
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	25	578.8	48.3	1015	3	US-09-015-734-1	Sequence 1, Appli
c	26	578.8	48.3	1015	3	US-09-015-734-3	Sequence 3, Appli
	27	578.8	48.3	1015	4	US-09-515-311-1	Sequence 1, Appli
c	28	578.8	48.3	1015	4	US-09-515-311-3	Sequence 3, Appli
	29	520.2	43.4	1069	2	US-08-768-964-1	Sequence 1, Appli
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	31	520.2	43.4	1069	3	US-09-005-299-1	Sequence 1, Appli
c	32	520.2	43.4	1069	3	US-09-005-299-3	Sequence 3, Appli
	33	520.2	43.4	1069	3	US-09-515-431-1	Sequence 1, Appli
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	40	435	36.3	765	4	US-09-515-311-4	Sequence 4, Appli
c	41	435	36.3	765	4	US-09-515-311-5	Sequence 5, Appli
	42	433.8	36.2	991	3	US-08-833-488B-19	Sequence 19, Appl
c	43	433.8	36.2	991	3	US-08-833-488B-21	Sequence 21, Appl
	44	403.8	33.7	708	3	US-09-015-734-6	Sequence 6, Appli
c	45	403.8	33.7	708	3	US-09-015-734-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-08-756-387B-1
; Sequence 1, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..877
US-08-756-387B-1

Query Match 100.0%; Score 1198; DB 2; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2.5e-292;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
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Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
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Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
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Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
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Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
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Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
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Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
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Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
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Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
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Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
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Db       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
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RESULT 2
US-08-756-387B-3/c
; Sequence 3, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-756-387B-3

Query Match 100.0%; Score 1198; DB 2; Length 1198;
Best Local Similarity 100.0%; Pred. No. 2.5e-292;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 1139

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 1079

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
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Db       1078 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 1019

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
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Db       1018 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 959
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Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 899

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 839

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
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Db        838 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 779

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
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Db        778 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 719

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
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Db        718 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 659

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
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Db        658 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 599

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
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Db        598 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 539

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
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Db        538 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 479

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
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Db        478 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 419

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
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Db        418 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 359

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
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Db        358 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 299

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
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Db        298 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 239

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
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Db        238 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 179

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
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Db        178 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 119

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
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Db        118 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 59

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
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Db          58 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAA 1

RESULT 3
US-09-285-873-1
; Sequence 1, Application US/09285873
; Patent No. 6309832
;  GENERAL INFORMATION:
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Porter, James P.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wassom, Donald L.
;    TITLE OF INVENTION:  Method to Detect IgE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carol Talkington Verser, Ph.D.
;      ADDRESSEE:  Heska Corporation
;      STREET:  1825 Sharp Point Drive
;      CITY:  Fort Collins
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80525
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect for Windows, Version 7.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/285,873
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/756,387
;      FILING DATE:  No. 6309832ember 26, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Verser, Carol Talkington
;      REGISTRATION NUMBER:  37,459
;      REFERENCE/DOCKET NUMBER:  DI-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  970/493-7272
;      TELEFAX:  970/484-9505
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1198 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  107..877
US-09-285-873-1

  Query Match           100.0%;  Score 1198;  DB 4;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-292;
  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
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Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
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Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
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Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
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Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
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Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
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Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
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Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
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Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
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Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
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Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
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Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
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Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
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Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
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RESULT 4
US-09-285-873-3/c
; Sequence 3, Application US/09285873
; Patent No. 6309832
;  GENERAL INFORMATION:
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Porter, James P.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wassom, Donald L.
;    TITLE OF INVENTION:  Method to Detect IgE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carol Talkington Verser, Ph.D.
;      ADDRESSEE:  Heska Corporation
;      STREET:  1825 Sharp Point Drive
;      CITY:  Fort Collins
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80525
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect for Windows, Version 7.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/285,873
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/756,387
;      FILING DATE:  No. 6309832ember 26, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Verser, Carol Talkington
;      REGISTRATION NUMBER:  37,459
;      REFERENCE/DOCKET NUMBER:  DI-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  970/493-7272
;      TELEFAX:  970/484-9505
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1198 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-285-873-3

  Query Match           100.0%;  Score 1198;  DB 4;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-292;
  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 1139

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 1079

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 1019

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 959

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 899

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 839

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 779

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        778 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 719

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 659

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 599

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
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Db        598 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 539

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
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Db        538 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 479

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
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Db        478 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 419

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 359

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 299

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 239

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 179

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 119

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 59

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
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Db          58 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
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RESULT 5
US-09-944-277A-1
; Sequence 1, Application US/09944277A
; Patent No. 6682894
;   GENERAL INFORMATION:
;        APPLICANT: Frank, Glenn R.
;                   Porter, James P.
;                   Rushlow, Keith E.
;                   Wassom, Donald L.
;        TITLE OF INVENTION: Method to Detect IgE
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Carol Talkington Verser, Ph.D.
;                        Heska Corporation
;             STREET: 1825 Sharp Point Drive
;             CITY: Fort Collins
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80525
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: WordPerfect for Windows, Version 7.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/944,277A
;             FILING DATE: 30-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/285,873
;             FILING DATE: 1999-03-31
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Verser, Carol Talkington
;             REGISTRATION NUMBER: 37,459
;             REFERENCE/DOCKET NUMBER: DI-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 970/493-7272
;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1198 nucleotides
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:   CDS
;             LOCATION:   107..877
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-944-277A-1

  Query Match             100.0%;  Score 1198;  DB 4;  Length 1198;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-292;
  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
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Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
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Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
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Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
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Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
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Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
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Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
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RESULT 6
US-09-944-277A-3/c
; Sequence 3, Application US/09944277A
; Patent No. 6682894
;   GENERAL INFORMATION:
;        APPLICANT: Frank, Glenn R.
;                   Porter, James P.
;                   Rushlow, Keith E.
;                   Wassom, Donald L.
;        TITLE OF INVENTION: Method to Detect IgE
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Carol Talkington Verser, Ph.D.
;                        Heska Corporation
;             STREET: 1825 Sharp Point Drive
;             CITY: Fort Collins
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80525
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: WordPerfect for Windows, Version 7.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/944,277A
;             FILING DATE: 30-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/285,873
;             FILING DATE: 1999-03-31
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Verser, Carol Talkington
;             REGISTRATION NUMBER: 37,459
;             REFERENCE/DOCKET NUMBER: DI-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 970/493-7272
;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1198 nucleotides
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-944-277A-3

  Query Match           100.0%;  Score 1198;  DB 4;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-292;
  Matches 1198;  Conservative    0;  Mismatches   0;  Indels    0;  Gaps    0;

Qy           1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1198 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 1139

Qy          61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
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Db        1138 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 1079

Qy         121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1078 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 1019

Qy         181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
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Db        1018 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 959

Qy         241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
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Db         958 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 899

Qy         301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
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Db         898 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 839

Qy         361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         838 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 779

Qy         421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         778 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 719

Qy         481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         718 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 659

Qy         541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
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Db         658 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 599

Qy         601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
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Db         598 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 539

Qy         661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         538 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 479

Qy         721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         478 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 419

Qy         781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         418 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 359

Qy         841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         358 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 299

Qy         901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         298 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 239
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Qy       961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
Db       238 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 179

Qy      1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
Db       178 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 119

Qy      1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
Db       118 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 59

Qy      1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
Db         58 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAA 1
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RESULT 7
US-07-869-933-10
; Sequence 10, Application US/07869933
; Patent No. 5770396
; GENERAL INFORMATION:
; APPLICANT: KINET, Jean-Pierre
; TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
; TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
; TITLE OF INVENTION: IMMUNOGLOBULIN
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/869,933
; FILING DATE: 19920416
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 40399/154 NIHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1174 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..880
US-07-869-933-10

Query Match 95.6%; Score 1144.8; DB 1; Length 1174;
Best Local Similarity 99.7%; Pred. No. 6.2e-279;
Matches 1157; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
Db       1081 GAATGAATAGATTCATTTATTAGCA-TTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1139

Qy       1141 TATAAAACCATGTAACAGAA 1160
Db       1140 TATAAAACCATGTAAAAAAA 1159
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RESULT 8
US-09-103-663-10
; Sequence 10, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
;  APPLICANT: Kinet et al.
;  TITLE OF INVENTION: Isolation, characterization, and use of the human beta
;  TITLE OF INVENTION: subunit of the high affinity receptor for
;  TITLE OF INVENTION: immunoglobulin E.
;  FILE REFERENCE: 50490
;  CURRENT APPLICATION NUMBER: US/09/103,663D
;  CURRENT FILING DATE: 1998-06-23
;  EARLIER APPLICATION NUMBER: 07/869,933
;  EARLIER FILING DATE: 1992-04-16
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 1174
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (107)..(880)
US-09-103-663-10

  Query Match             95.6%;  Score 1144.8;  DB 3;  Length 1174;
  Best Local Similarity   99.7%;  Pred. No. 6.2e-279;
  Matches 1157;  Conservative    0;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540

Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600

Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660

Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720

Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780

Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840

Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900

Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960

Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020

Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db       1081 GAATGAATAGATTCATTTATTAGCA-TTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1139

Qy       1141 TATAAAACCATGTAACAGAA 1160
              |||||||||||||| | ||
Db       1140 TATAAAACCATGTAAAAAAA 1159


RESULT 9
US-08-756-387B-4
; Sequence 4, Application US/08756387B
; Patent No. 5945294
;  GENERAL INFORMATION:
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Porter, James P.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wassom, Donald L.
;    TITLE OF INVENTION:  Method to Detect IgE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carol Talkington Verser, Ph.D.
;      ADDRESSEE:  Heska Corporation
;      STREET:  1825 Sharp Point Drive
;      CITY:  Fort Collins
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80525
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect for Windows, Version 7.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/756,387B
;      FILING DATE:  No. 5945294ember 26, 1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Verser, Carol Talkington
;      REGISTRATION NUMBER:  37,459
;      REFERENCE/DOCKET NUMBER:  DI-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  970/493-7272
```

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;      TELEFAX:  970/484-9505
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  774 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..774
US-08-756-387B-4

  Query Match             64.6%;  Score 774;  DB 2;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-185;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60

Qy        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120

Qy        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180

Qy        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240

Qy        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300

Qy        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360

Qy        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420

Qy        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480

Qy        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540

Qy        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600

Qy        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660

Qy        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720

Qy        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774


RESULT 10
US-08-756-387B-5/c
; Sequence 5, Application US/08756387B
; Patent No. 5945294
;  GENERAL INFORMATION:
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Porter, James P.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wassom, Donald L.
;    TITLE OF INVENTION:  Method to Detect IgE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carol Talkington Verser, Ph.D.
;      ADDRESSEE:  Heska Corporation
;      STREET:  1825 Sharp Point Drive
;      CITY:  Fort Collins
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80525
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect for Windows, Version 7.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/756,387B
;      FILING DATE:  No. 5945294ember 26, 1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Verser, Carol Talkington
;      REGISTRATION NUMBER:  37,459
;      REFERENCE/DOCKET NUMBER:  DI-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  970/493-7272
;      TELEFAX:  970/484-9505
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  774 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-756-387B-5

  Query Match             64.6%;  Score 774;  DB 2;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-185;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 715

Qy        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 655

Qy        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 595

Qy        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 535

Qy        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 475

Qy        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 415

Qy        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 355
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Qy        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 295

Qy        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 235

Qy        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 175

Qy        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 115

Qy        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 55

Qy        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         54 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 1
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RESULT 11
US-09-285-873-4
; Sequence 4, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 774 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..774

US-09-285-873-4

Query Match 64.6%; Score 774; DB 4; Length 774;
Best Local Similarity 100.0%; Pred. No. 1.3e-185;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60

Qy        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120

Qy        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180

Qy        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240

Qy        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300

Qy        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360

Qy        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420

Qy        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480

Qy        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540

Qy        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600

Qy        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660

Qy        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720

Qy        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
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RESULT 12
US-09-285-873-5/c
; Sequence 5, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation

```
;       STREET:  1825 Sharp Point Drive
;       CITY:  Fort Collins
;       STATE:  Colorado
;       COUNTRY:  USA
;       ZIP:  80525
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  Windows 95
;       SOFTWARE:  WordPerfect for Windows, Version 7.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/285,873
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/756,387
;       FILING DATE:  No. 6309832ember 26, 1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Verser, Carol Talkington
;       REGISTRATION NUMBER:  37,459
;       REFERENCE/DOCKET NUMBER:  DI-1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  970/493-7272
;       TELEFAX:  970/484-9505
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  774 nucleotides
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-09-285-873-5

  Query Match             64.6%;  Score 774;  DB 4;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-185;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 715

Qy        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 655

Qy        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 595

Qy        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 535

Qy        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 475

Qy        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 415

Qy        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 355

Qy        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 295

Qy        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 235

Qy        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 175

Qy        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 115

Qy        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 55

Qy        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         54 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 1


RESULT 13
US-09-944-277A-4
; Sequence 4, Application US/09944277A
; Patent No. 6682894
;   GENERAL INFORMATION:
;       APPLICANT: Frank, Glenn R.
;                  Porter, James P.
;                  Rushlow, Keith E.
;                  Wassom, Donald L.
;       TITLE OF INVENTION: Method to Detect IgE
;       NUMBER OF SEQUENCES: 13
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Carol Talkington Verser, Ph.D.
;                       Heska Corporation
;            STREET: 1825 Sharp Point Drive
;            CITY: Fort Collins
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80525
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: Windows 95
;            SOFTWARE: WordPerfect for Windows, Version 7.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/944,277A
;            FILING DATE: 30-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/285,873
;            FILING DATE: 1999-03-31
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Verser, Carol Talkington
;            REGISTRATION NUMBER: 37,459
;            REFERENCE/DOCKET NUMBER: DI-1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 970/493-7272
;            TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 774 nucleotides
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:   CDS
;            LOCATION:   1..774
;       SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-944-277A-4

  Query Match             64.6%;  Score 774;  DB 4;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-185;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166
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Db          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60

Qy        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120

Qy        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180

Qy        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240

Qy        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300

Qy        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360

Qy        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420

Qy        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480

Qy        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540

Qy        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600

Qy        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660

Qy        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720

Qy        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774


RESULT 14
US-09-944-277A-5/c
; Sequence 5, Application US/09944277A
; Patent No. 6682894
;   GENERAL INFORMATION:
;        APPLICANT: Frank, Glenn R.
;                   Porter, James P.
;                   Rushlow, Keith E.
;                   Wassom, Donald L.
;        TITLE OF INVENTION: Method to Detect IgE
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Carol Talkington Verser, Ph.D.
;                        Heska Corporation
;             STREET: 1825 Sharp Point Drive
;             CITY: Fort Collins
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80525
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: WordPerfect for Windows, Version 7.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/944,277A
;             FILING DATE: 30-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/285,873
;             FILING DATE: 1999-03-31
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Verser, Carol Talkington
;             REGISTRATION NUMBER: 37,459
;             REFERENCE/DOCKET NUMBER: DI-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 970/493-7272
;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 774 nucleotides
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-944-277A-5

  Query Match             64.6%;  Score 774;  DB 4;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-185;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 715

Qy        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 655

Qy        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286
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Db        654 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 595

Qy        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 535

Qy        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 475

Qy        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 415

Qy        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 355

Qy        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 235

Qy        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 175

Qy        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        174 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 115

Qy        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 55

Qy        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         54 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 1


RESULT 15
US-08-897-956A-6
; Sequence 6, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
;  APPLICANT:  Mary Ellen Digan
;  APPLICANT:  Philip Lake
;  APPLICANT:  Hermann Gram
;  TITLE OF INVENTION:  Fusion Polypeptides
;  FILE REFERENCE:  600-7244/CPA
;  CURRENT APPLICATION NUMBER: US/08/897,956A
;  CURRENT FILING DATE:  1997-07-21
;  PRIOR APPLICATION NUMBER:  60/022,689
;  PRIOR FILING DATE:  1996-07-26
;  NUMBER OF SEQ ID NOS:  38
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 6
;   LENGTH: 773
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion Polynucleotide
US-08-897-956A-6

  Query Match             64.5%;  Score 773;  DB 4;  Length 773;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-185;
  Matches  773;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60

Qy        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120

Qy        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180

Qy        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240

Qy        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300

Qy        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466
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Db        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360

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GenCore version 5.1.6

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Perfect score: 1198
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	2	1198	100.0	1198	9	US-09-944-277A-3	Sequence 3, Appli
	3	1198	100.0	1198	9	US-09-962-832-244	Sequence 244, App
	4	1198	100.0	1198	17	US-10-775-169-141	Sequence 141, App
	5	882.8	73.7	898	13	US-10-236-392-27	Sequence 27, Appl
	6	774	64.6	774	9	US-09-944-277A-4	Sequence 4, Appli
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	8	699	58.3	699	9	US-09-944-277A-7	Sequence 7, Appli
	9	630	52.6	757	13	US-10-236-392-29	Sequence 29, Appl
	10	591	49.3	591	9	US-09-944-277A-10	Sequence 10, Appl
	11	578.8	48.3	1015	16	US-10-434-817-1	Sequence 1, Appli
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	26	167.8	14.0	887	17	US-10-641-643-1287	Sequence 1287, Ap
	27	166.2	13.9	887	16	US-10-191-997-124	Sequence 124, App
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	33	163	13.6	1977	13	US-10-240-425-1268	Sequence 1268, Ap
	34	163	13.6	1977	13	US-10-342-887-382	Sequence 382, App
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	43	139.6	11.7	1321	13	US-10-172-118-1906	Sequence 1906, Ap
	44	139.2	11.6	1398	9	US-09-925-301-286	Sequence 286, App
	45	138	11.5	1035	15	US-10-384-850-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1
US-09-944-277A-1
; Sequence 1, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272

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;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1198 nucleotides
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:   CDS
;             LOCATION:   107..877
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-944-277A-1

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  Best Local Similarity  100.0%;  Pred. No. 1.9e-288;
  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
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; Sequence 3, Application US/09944277A
; Patent No. US20020034771A1
;   GENERAL INFORMATION:
;        APPLICANT: Frank, Glenn R.
;                   Porter, James P.
;                   Rushlow, Keith E.
;                   Wassom, Donald L.
;        TITLE OF INVENTION: Method to Detect IgE
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Carol Talkington Verser, Ph.D.
;                        Heska Corporation
;             STREET: 1825 Sharp Point Drive
;             CITY: Fort Collins
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80525
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: WordPerfect for Windows, Version 7.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/944,277A
;             FILING DATE: 30-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/285,873
;             FILING DATE: 1999-03-31
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Verser, Carol Talkington
;             REGISTRATION NUMBER: 37,459
;             REFERENCE/DOCKET NUMBER: DI-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 970/493-7272
;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1198 nucleotides
;             TYPE: nucleic acid
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Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 119

Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 59

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          58 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1
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RESULT 3
US-09-962-832-244
; Sequence 244, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
;  APPLICANT: Ebner, Reinhard
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-74
;  CURRENT APPLICATION NUMBER: US/09/962,832
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,077
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,280
;  PRIOR FILING DATE: 2000-09-25
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 244
;   LENGTH: 1198
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-962-832-244

  Query Match             100.0%;  Score 1198;  DB 9;  Length 1198;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-288;
  Matches 1198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60

Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120

Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180

Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240

Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300

Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360

Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420

Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480

Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
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Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
Db       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
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RESULT 4
US-10-775-169-141
; Sequence 141, Application US/10775169
; Publication No. US20040175743A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dorner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
; LENGTH: 1198
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-141

Query Match 100.0%; Score 1198; DB 17; Length 1198;
Best Local Similarity 100.0%; Pred. No. 1.9e-288;
Matches 1198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
Db          1 TACTAAGAGTCTCCAGCATCCTCCACCTGTCTACCACCGAGCATGGGCCTATATTTGAAG 60
Qy         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
Db         61 CCTTAGATCTCTCCAGCACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCAT 120
Qy        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
Db        121 GGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGC 180
Qy        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
Db        181 AGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGA 240
Qy        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
Db        241 GAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTT 300
Qy        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
Db        301 CCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATT 360
Qy        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
Db        361 TGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTA 420
Qy        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
Db        421 CCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGG 480
Qy        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
Db        481 CCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTA 540
Qy        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
Db        541 TTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAA 600
Qy        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
Db        601 TGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTA 660
Qy        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
Db        661 TGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACA 720
Qy        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
Db        721 ATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTC 780
Qy        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
Db        781 AACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACT 840
Qy        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
Db        841 TCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATAT 900
Qy        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
Db        901 TTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTG 960
Qy        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
Db        961 CAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTG 1020
Qy       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
Db       1021 AAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGA 1080
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Qy       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 GAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAA 1140

Qy       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TATAAAACCATGTAACAGAATGCTTCTGAGTAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1198


RESULT 5
US-10-236-392-27
; Sequence 27, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, David W
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Burgess, Catherine, E
;  APPLICANT:  Casman, Stacie J
;  APPLICANT:  Catterton, Elina
;  APPLICANT:  Chapoval, Andrei
;  APPLICANT:  Crabtree, Julie
;  APPLICANT:  Edinger, Shlomit, R
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Gusev, Vladamir
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  LaRochelle, William J
;  APPLICANT:  Li, Li
;  APPLICANT:  MacDougall, John R
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Miller, Charles E
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Pena, Carol A
;  APPLICANT:  Peyman, John A
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Reiger, Daniel K
;  APPLICANT:  Rothenberg, Mark E
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-442A
;  CURRENT APPLICATION NUMBER: US/10/236,392
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US09/540,763
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: US60/390,155
;  PRIOR FILING DATE: 2002-06-19
;  PRIOR APPLICATION NUMBER: US09/635,949
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: US60/318,765
;  PRIOR FILING DATE: 2001-09-12
;  PRIOR APPLICATION NUMBER: US60/357,303
;  PRIOR FILING DATE: 2002-02-15
;  PRIOR APPLICATION NUMBER: US60/367,753
;  PRIOR FILING DATE: 2002-03-25
;  PRIOR APPLICATION NUMBER: US60/369,479
;  PRIOR FILING DATE: 2002-04-02
;  PRIOR APPLICATION NUMBER: US09/659,634
;  PRIOR FILING DATE: 2000-09-12
;  PRIOR APPLICATION NUMBER: US60/318,120
;  PRIOR FILING DATE: 2001-09-07
;  PRIOR APPLICATION NUMBER: US60/318,130
;  PRIOR FILING DATE: 2001-09-07
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 794
;  SOFTWARE: Custom
; SEQ ID NO 27
;   LENGTH: 898
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (26)..(797)
US-10-236-392-27

  Query Match            73.7%;  Score 882.8;  DB 13;  Length 898;
  Best Local Similarity  99.8%;  Pred. No. 8.4e-210;
  Matches  884;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         82 TAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTACTGTG 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTACTGTG 60

Qy        142 TGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGT 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGT 120

Qy        202 CTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTACATGTAA 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTACATGTAA 180

Qy        262 TGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTTCAGA 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTTCAGA 240

Qy        322 AGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAATACAA 381
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAATACAA 300

Qy        382 ATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTG 360

Qy        442 GCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTG 420

Qy        502 CCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCT 561
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCT 480

Qy        562 CAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGG 621
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGG 540

Qy        622 AACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACAT 681
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACAT 600

Qy        682 TACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGT 741
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGT 660

Qy        742 GGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATT 801
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        661 GGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACCCAGCAGCAGGTCACATT 720

Qy        802 TCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCC 861
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCC 780

Qy        862 AAACCCCAAAAACAACTGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCC 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAACCCCAAAAACAACTGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCC 840

Qy        922 AGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATATA 967
              |||||||||||||||||||||||||||||||||||||||||||| |
Db        841 AGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATAAA 886


RESULT 6
```

```
US-09-944-277A-4
; Sequence 4, Application US/09944277A
; Patent No. US20020034771A1
;  GENERAL INFORMATION:
;       APPLICANT: Frank, Glenn R.
;                  Porter, James P.
;                  Rushlow, Keith E.
;                  Wassom, Donald L.
;       TITLE OF INVENTION: Method to Detect IgE
;       NUMBER OF SEQUENCES: 13
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Carol Talkington Verser, Ph.D.
;                       Heska Corporation
;            STREET: 1825 Sharp Point Drive
;            CITY: Fort Collins
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80525
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: Windows 95
;            SOFTWARE: WordPerfect for Windows, Version 7.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/944,277A
;            FILING DATE: 30-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/285,873
;            FILING DATE: 1999-03-31
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Verser, Carol Talkington
;            REGISTRATION NUMBER: 37,459
;            REFERENCE/DOCKET NUMBER: DI-1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 970/493-7272
;            TELEFAX: 970/484-9505
;  INFORMATION FOR SEQ ID NO: 4:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 774 nucleotides
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:   CDS
;            LOCATION:   1..774
;       SEQUENCE DESCRIPTION: SEQ ID NO:4:
US-09-944-277A-4

  Query Match             64.6%;  Score 774;  DB 9;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-182;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60

Qy        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120

Qy        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180

Qy        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240

Qy        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300

Qy        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360

Qy        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420

Qy        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480

Qy        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540

Qy        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600

Qy        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660

Qy        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720

Qy        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774


RESULT 7
US-09-944-277A-5/c
; Sequence 5, Application US/09944277A
; Patent No. US20020034771A1
;  GENERAL INFORMATION:
;       APPLICANT: Frank, Glenn R.
;                  Porter, James P.
;                  Rushlow, Keith E.
;                  Wassom, Donald L.
;       TITLE OF INVENTION: Method to Detect IgE
;       NUMBER OF SEQUENCES: 13
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Carol Talkington Verser, Ph.D.
;                       Heska Corporation
;            STREET: 1825 Sharp Point Drive
;            CITY: Fort Collins
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80525
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: Windows 95
;            SOFTWARE: WordPerfect for Windows, Version 7.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/944,277A
;            FILING DATE: 30-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/285,873
;            FILING DATE: 1999-03-31
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Verser, Carol Talkington
;            REGISTRATION NUMBER: 37,459
;            REFERENCE/DOCKET NUMBER: DI-1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 970/493-7272
;            TELEFAX: 970/484-9505
;  INFORMATION FOR SEQ ID NO: 5:
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;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 774 nucleotides
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-944-277A-5

  Query Match             64.6%;  Score 774;  DB 9;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-182;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 715

Qy        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 655

Qy        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 595

Qy        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 535

Qy        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 475

Qy        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 415

Qy        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 355

Qy        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 295

Qy        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 235

Qy        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 175

Qy        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 115

Qy        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 55

Qy        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         54 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 1


RESULT 8
US-09-944-277A-7
; Sequence 7, Application US/09944277A
; Patent No. US20020034771A1
;   GENERAL INFORMATION:
;       APPLICANT: Frank, Glenn R.
;                  Porter, James P.
;                  Rushlow, Keith E.
;                  Wassom, Donald L.
;       TITLE OF INVENTION: Method to Detect IgE
;       NUMBER OF SEQUENCES: 13
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Carol Talkington Verser, Ph.D.
;                       Heska Corporation
;            STREET: 1825 Sharp Point Drive
;            CITY: Fort Collins
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80525
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: Windows 95
;            SOFTWARE: WordPerfect for Windows, Version 7.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/944,277A
;            FILING DATE: 30-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/285,873
;            FILING DATE: 1999-03-31
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Verser, Carol Talkington
;            REGISTRATION NUMBER: 37,459
;            REFERENCE/DOCKET NUMBER: DI-1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 970/493-7272
;            TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 699 nucleotides
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:   CDS
;            LOCATION:   1..699
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-944-277A-7

  Query Match             58.3%;  Score 699;  DB 9;  Length 699;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-164;
  Matches  699;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        182 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 60

Qy        242 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 120

Qy        302 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 180

Qy        362 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240

Qy        422 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 300

Qy        482 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 360

Qy        542 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 601
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 420

Qy        602 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 661
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 480

Qy        662 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAA 721
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAA 540

Qy        722 TTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCA 781
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCA 600

Qy        782 ACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTT 841
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTT 660

Qy        842 CTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
                ||||||||||||||||||||||||||||||||||||||
Db        661 CTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 699


RESULT 9
US-10-236-392-29
; Sequence 29, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, David W
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Burgess, Catherine, E
;  APPLICANT:  Casman, Stacie J
;  APPLICANT:  Catterton, Elina
;  APPLICANT:  Chapoval, Andrei
;  APPLICANT:  Crabtree, Julie
;  APPLICANT:  Edinger, Shlomit, R
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Gusev, Vladamir
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  LaRochelle, William J
;  APPLICANT:  Li, Li
;  APPLICANT:  MacDougall, John R
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Miller, Charles E
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Pena, Carol A
;  APPLICANT:  Peyman, John A
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Reiger, Daniel K
;  APPLICANT:  Rothenberg, Mark E
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-442A
;  CURRENT APPLICATION NUMBER: US/10/236,392
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US09/540,763
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: US60/390,155
;  PRIOR FILING DATE: 2002-06-19
;  PRIOR APPLICATION NUMBER: US09/635,949
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: US60/318,765
;  PRIOR FILING DATE: 2001-09-12
;  PRIOR APPLICATION NUMBER: US60/357,303
;  PRIOR FILING DATE: 2002-02-15
;  PRIOR APPLICATION NUMBER: US60/367,753
;  PRIOR FILING DATE: 2002-03-25
;  PRIOR APPLICATION NUMBER: US60/369,479
;  PRIOR FILING DATE: 2002-04-02
;  PRIOR APPLICATION NUMBER: US09/659,634
;  PRIOR FILING DATE: 2000-09-12
;  PRIOR APPLICATION NUMBER: US60/318,120
;  PRIOR FILING DATE: 2001-09-07
;  PRIOR APPLICATION NUMBER: US60/318,130
;  PRIOR FILING DATE: 2001-09-07
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 794
;  SOFTWARE: Custom
; SEQ ID NO 29
;   LENGTH: 757
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (26)..(680)
US-10-236-392-29

  Query Match             52.6%;  Score 630;  DB 13;  Length 757;
  Best Local Similarity   86.6%;  Pred. No. 1e-146;
  Matches  757;  Conservative    0;  Mismatches    0;  Indels  117;  Gaps    1;

Qy         82 TAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTACTGTG 141
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTACTGTG 60

Qy        142 TGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGT 201
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGT 120

Qy        202 CTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTACATGTAA 261
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTACATGTAA 180

Qy        262 TGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTTCAGA 321
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTTCAGA 240

Qy        322 AGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAATACAA 381
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAATACAA 300

Qy        382 ATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTG 441
               |
Db        301 A---------------------------------------------------------- 301

Qy        442 GCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTG 501
                                                                        ||
Db        302 ----------------------------------------------------------TG 303

Qy        502 CCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCT 561
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 CCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCT 363

Qy        562 CAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGG 621
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 CAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGG 423

Qy        622 AACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACAT 681
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACAT 483

Qy        682 TACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGT 741
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 TACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGT 543

Qy        742 GGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATT 801
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        544 GGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATT 603
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Qy        802 TCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCC 861
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Db        604 TCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCC 663

Qy        862 AAACCCCAAAAACAACTGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCC 921
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 AAACCCCAAAAACAACTGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCC 723

Qy        922 AGCATCAGCAATTGCTACTCAATTGTCAAACACA 955
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Db        724 AGCATCAGCAATTGCTACTCAATTGTCAAACACA 757


RESULT 10
US-09-944-277A-10
; Sequence 10, Application US/09944277A
; Patent No. US20020034771A1
;   GENERAL INFORMATION:
;        APPLICANT: Frank, Glenn R.
;                   Porter, James P.
;                   Rushlow, Keith E.
;                   Wassom, Donald L.
;        TITLE OF INVENTION: Method to Detect IgE
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Carol Talkington Verser, Ph.D.
;                        Heska Corporation
;             STREET: 1825 Sharp Point Drive
;             CITY: Fort Collins
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80525
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: WordPerfect for Windows, Version 7.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/944,277A
;             FILING DATE: 30-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/285,873
;             FILING DATE: 1999-03-31
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Verser, Carol Talkington
;             REGISTRATION NUMBER: 37,459
;             REFERENCE/DOCKET NUMBER: DI-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 970/493-7272
;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 nucleotides
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:   CDS
;             LOCATION:   1..591
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-944-277A-10

  Query Match             49.3%;  Score 591;  DB 9;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 4.8e-137;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60

Qy        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120

Qy        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180

Qy        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240

Qy        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406
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Db        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300

Qy        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360

Qy        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420

Qy        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480

Qy        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540

Qy        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCT 697
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCT 591


RESULT 11
US-10-434-817-1
; Sequence 1, Application US/10434817
; Publication No. US20030235579A1
;   GENERAL INFORMATION:
;        APPLICANT: Weber, Eric R.
;                   McCall, Catherine A.
;        TITLE OF INVENTION: NOVEL EQUINE Fc EPSILON RECEPTOR ALPHA
;                            CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Heska Corporation
;             STREET: 1825 Sharp Point Drive
;             CITY: Fort Collins
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80525
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WordPerfect for Windows, Version 7.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/434,817
;             FILING DATE: 08-May-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/015,734
;             FILING DATE: 29-JAN-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Verser, Carol Talkington
;             REGISTRATION NUMBER: 37,459
;             REFERENCE/DOCKET NUMBER: DI-4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 970/493-7272
;             TELEFAX: 970/484-9505
;
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;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1015 nucleotides
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:   CDS
;             LOCATION:   12..776
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-434-817-1

  Query Match            48.3%;  Score 578.8;  DB 16;  Length 1015;
  Best Local Similarity  75.5%;  Pred. No. 7.4e-134;
  Matches  764;  Conservative    0;  Mismatches  232;  Indels   16;  Gaps    3;

Qy         96 CCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGT 155
Db          1 CCACAGAGGAGATGCCTGCTCCCATGGGAAGCCCTGCCCTGCTGTGGATAACTTTTCTGC 60

Qy        156 TCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTC 215
Db         61 TCTTCTCTCTGGATGGCGTGCCAGCAGCCATCCGGAAATCTACAGTGTCCTTGAATCCCC 120

Qy        216 CATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCT 275
Db        121 CATGGAATAGAATATTTCGAGGAGAGAATGTGACTCTTACATGTAATAAGAACAAGCCCC 180

Qy        276 TTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAA 335
Db        181 TTAAAGGCAACTCCACTGAGTGGACCTACAACAACACCACTTTAGAAGTGACAACTTCAA 240

Qy        336 GTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAAC 395
Db        241 GTTTGAACATCACTAATGCCTCACACCGGAGCAGTGGGGAATACAGATGTCGGAACAATG 300

Qy        396 AAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGG 455
Db        301 ACTTGAACCTGAGTGAAGCTGTGCACCTAGAAGTTTTCAGTGACTGGCTGCTCCTTCAGG 360

Qy        456 CCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGA 515
Db        361 CCTCTGCTGAGGAGGTCATAGAGGGTAAGGCCCTCGTTCTCAGGTGCCGTGGCTGGAAGG 420

Qy        516 ACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATG 575
Db        421 ATTGGGACGTCTTCAAGGTGATCTACTACAAGGATGGCAAACCCCTCGAGTACTGGTATG 480

Qy        576 AGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTA 635
Db        481 AGAACAAAAACATCTCCATTGAAAGTGCCACAACAGAAAACAGTGGCACCTATTACTGCG 540

Qy        636 CGGG----------CAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTA 683
Db        541 AGGGTGCTTTTAACTTTAAGCGAACAAGTGAACGCTATACCTCTGATTACCTCAACATTA 600

Qy        684 CTGTAATAAAAGCTCCGC---GTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGG 740
Db        601 CTGTAAAAAAAGCTGAGCAAAGCAAACGCTACTGGCTACAATTTATTATTCCATTGTTGG 660

Qy        741 TGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACAT 800
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Qy        801 TTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCC-TAAG 859
Db        721 TTCTCTTGAAGATTAAGAGGACCAGGAGAGGCAGAAAACTTATGGACCCCCATCCTTAAG 780

Qy        860 CCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTT 919
Db        781 TGAGACCCGAGAAAGAACTGATGTCACTGCTCAAGAAACCTTTGCAACAGCAATTTCTTC 840

Qy        920 CCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATATACATAGAAACGTC 979
Db        841 CTGGCATCAGCAATTGCTTTTCAGTTGTCAAACACAGATCATAATGTACATAGAAAGGTC 900

Qy        980 TGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTAAGTGGCATG 1039
Db        901 TATGCCCACGGCTTTGCAGAATTGCATCATTAAACTAACTAGAACTGGTTAAGTGGCATG 960

Qy       1040 TAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAATGAATAGA 1091
Db        961 TAATAGTAAGTGCTCAATAAACATCATTTAAATAAATATAAAAAAAAAAAAA 1012


RESULT 12
US-10-434-817-3/c
; Sequence 3, Application US/10434817
; Publication No. US20030235579A1
;   GENERAL INFORMATION:
;        APPLICANT: Weber, Eric R.
;                   McCall, Catherine A.
;        TITLE OF INVENTION: NOVEL EQUINE Fc EPSILON RECEPTOR ALPHA
;                            CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Heska Corporation
;             STREET: 1825 Sharp Point Drive
;             CITY: Fort Collins
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80525
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WordPerfect for Windows, Version 7.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/434,817
;             FILING DATE: 08-May-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/015,734
;             FILING DATE: 29-JAN-1998
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Verser, Carol Talkington
;             REGISTRATION NUMBER: 37,459
;             REFERENCE/DOCKET NUMBER: DI-4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 970/493-7272
;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1015 nucleotides
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-434-817-3

  Query Match            48.3%;  Score 578.8;  DB 16;  Length 1015;
  Best Local Similarity  75.5%;  Pred. No. 7.4e-134;
  Matches  764;  Conservative    0;  Mismatches  232;  Indels   16;  Gaps    3;

Qy         96 CCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGT 155
Db       1015 CCACAGAGGAGATGCCTGCTCCCATGGGAAGCCCTGCCCTGCTGTGGATAACTTTTCTGC 956

Qy        156 TCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTC 215
Db        955 TCTTCTCTCTGGATGGCGTGCCAGCAGCCATCCGGAAATCTACAGTGTCCTTGAATCCCC 896

Qy        216 CATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCT 275
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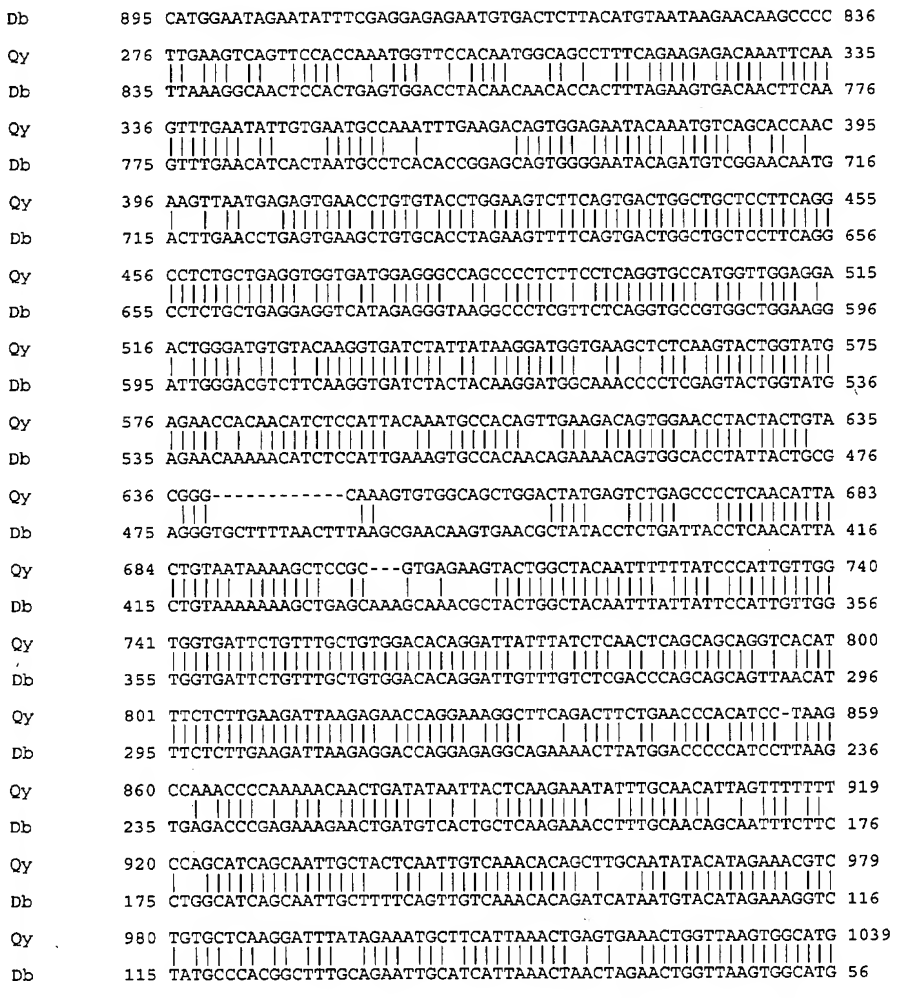
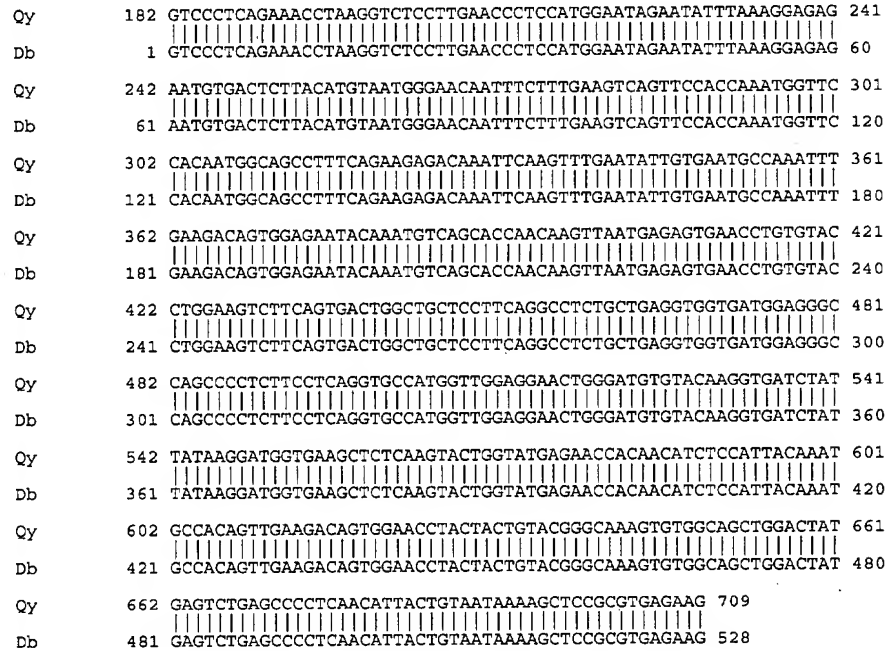


RESULT 13
US-09-809-715-1
; Sequence 1, Application US/09809715
; Publication No. US20030003502A1
; GENERAL INFORMATION:
; APPLICANT: Jardetzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Wurzburg, Beth A.
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A Fc
; TITLE OF INVENTION: EPSILON RECEPTOR ALPHA CHAIN AND A Fc REGION OF AN IgE
; TITLE OF INVENTION: ANTIBODY AND USES THEREOF
; FILE REFERENCE: AL-8
; CURRENT APPLICATION NUMBER: US/09/809,715
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/189,853
; PRIOR FILING DATE: 2000-03-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 528
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(528)
US-09-809-715-1

Query Match 44.1%; Score 528; DB 10; Length 528;
Best Local Similarity 100.0%; Pred. No. 2.4e-121;
Matches 528; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



RESULT 14
US-10-293-992-1
; Sequence 1, Application US/10293992
; Publication No. US20040033527A1
; GENERAL INFORMATION:
; APPLICANT: Jardetzky, Theodore S.
; APPLICANT: Garman, Scott Clayton
; APPLICANT: Kinet, Jean-Pierre
; TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A Fc EPSILON RECEPI
; TITLE OF INVENTION: CHAIN
; FILE REFERENCE: AL-3-C1-1
; CURRENT APPLICATION NUMBER: US/10/293,992
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 09/434,193
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/107,219
; PRIOR FILING DATE: 1998-11-05
; NUMBER OF SEQ ID NOS: 6

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;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 528
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(528)
;   OTHER INFORMATION:
US-10-293-992-1

  Query Match             44.1%;  Score 528;  DB 13;  Length 528;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-121;
  Matches  528;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        182 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 60

Qy        242 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 120

Qy        302 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 180

Qy        362 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240

Qy        422 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 300

Qy        482 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 360

Qy        542 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 601
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 420

Qy        602 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 480

Qy        662 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAG 709
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAG 528


RESULT 15
US-09-944-277A-12
; Sequence 12, Application US/09944277A
; Patent No. US20020034771A1
;   GENERAL INFORMATION:
;        APPLICANT: Frank, Glenn R.
;                   Porter, James P.
;                   Rushlow, Keith E.
;                   Wassom, Donald L.
;        TITLE OF INVENTION: Method to Detect IgE
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Carol Talkington Verser, Ph.D.
;                        Heska Corporation
;             STREET: 1825 Sharp Point Drive
;             CITY: Fort Collins
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80525
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: WordPerfect for Windows, Version 7.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/944,277A
;             FILING DATE: 30-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/285,873
;             FILING DATE: 1999-03-31
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Verser, Carol Talkington
;             REGISTRATION NUMBER: 37,459
;             REFERENCE/DOCKET NUMBER: DI-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 970/493-7272
;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 12:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 516 nucleotides
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:   CDS
;             LOCATION:   1..516
;        SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-944-277A-12

  Query Match             43.1%;  Score 516;  DB 9;  Length 516;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-118;
  Matches  516;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        182 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 241
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Db          1 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 60

Qy        242 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 301
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Db         61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 120

Qy        302 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 361
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 180

Qy        362 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 421
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240

Qy        422 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 300

Qy        482 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 541
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 360

Qy        542 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 601
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Db        361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 420

Qy        602 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 661
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 480

Qy        662 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCT 697
              |||||||||||||||||||||||||||||||||||
Db        481 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCT 516


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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	5	640	53.4	669	10	AW612525	AW612525 hh03f07.x
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c	15	455	38.0	479	10	BF593204	BF593204 7o50c04.x
c	16	441.2	36.8	446	9	AI676097	AI676097 wc05c12.x
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c	24	224	18.7	264	9	AI765235	AI765235 wi72h07.x
	25	222.8	18.6	394	10	AW357271	AW357271 40240 MAR
	26	218.8	18.3	422	10	BF603113	BF603113 268539 MA
	27	201.8	16.8	255	12	BM966772	BM966772 ij26c12.y
	28	199.2	16.6	483	13	BY593556	BY593556 BY593556
	29	175.8	14.7	403	14	CB768694	CB768694 AMGNNUC:S
	30	174.4	14.6	1201	9	AL514096	AL514096 AL514096
	31	172.8	14.4	438	13	BY585428	BY585428 BY585428
	32	172.4	14.4	429	13	BY228345	BY228345 BY228345
	33	169.8	14.2	848	14	CB958187	CB958187 AGENCOURT
	34	169.4	14.1	1033	9	AL549464	AL549464 AL549464
	35	169.4	14.1	1201	9	AL531122	AL531122 AL531122
	36	167.8	14.0	874	14	CD244068	CD244068 AGENCOURT
	37	167.8	14.0	1201	13	BX399366	BX399366 BX399366
	38	164.8	13.8	528	14	CB152997	CB152997 K-EST0210
	39	163.8	13.7	823	12	BI768140	BI768140 603056571
	40	163	13.6	1201	13	BX402696	BX402696 BX402696
	41	162.6	13.6	403	13	BY228552	BY228552 BY228552
	42	162.6	13.6	404	13	BY227642	BY227642 BY227642
	43	162.6	13.6	1201	9	AL558081	AL558081 AL558081
	44	162.2	13.5	664	14	CB555672	CB555672 MMSP0057_
	45	162.2	13.5	987	13	BX345202	BX345202 BX345202

ALIGNMENTS

RESULT 1
BQ573778/c
LOCUS BQ573778 768 bp mRNA linear EST 19-JUN-2002
DEFINITION UI-H-EZ0-bav-1-04-0-UI.s1 NCI_CGAP_Ch1 Homo sapiens cDNA clone UI-H-EZ0-bav-1-04-0-UI 3', mRNA sequence.
ACCESSION BQ573778
VERSION BQ573778.1 GI:21477095
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 768)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of Orthoapedics
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA

```
            sequence: 1-41, >AT_rich#Low_complexity (matched compliment)
            93-129, >LINE2 (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .768
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-EZ0-bav-1-04-0-UI"
                     /tissue_type="Chondrosarcoma Grade II"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_Ch1"
                     /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                     with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_Ch1 is a cDNA library containing the following
                     tissue(s): Chondrosarcoma Grade II. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     TGATCACGCT.
                     TAG_TISSUE=grade-2-chondrosarcoma
                     TAG_LIB=UI-H-EZ0
                     TAG_SEQ=ATCTAATATG"
ORIGIN

  Query Match             62.7%;  Score 750.6;  DB 13;  Length 768;
  Best Local Similarity   99.3%;  Pred. No. 6e-107;
  Matches  753;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        403 TGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGC 462
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        768 TGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGC 709

Qy        463 TGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGA 522
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        708 TGAGGTGGTGATGGAGGNCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGA 649

Qy        523 TGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCA 582
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        648 TGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCA 589

Qy        583 CAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAA 642
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 CAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAA 529

Qy        643 AGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCG 702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 AGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCG 469

Qy        703 TGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGA 762
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        468 TGAGAAGTACTGGCTACAATTTTTTATCCCATTCTTGGTGGTGATTCTGTTTGCTGTGGA 409

Qy        763 CACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAAC 822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAAC 349

Qy        823 CAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATA 882
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 CAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATA 289

Qy        883 TAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCA 942
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        288 TAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCA 229

Qy        943 ATTGTCAAACACAGCTTGCAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAAT 1002
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        228 ATTGTCAAACACAGCTTGCAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAAT 169

Qy       1003 GCTTCATTAAACTGAGTGAAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACA 1062
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        168 GCTTCATTAAACTGAGTGAAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACA 109

Qy       1063 TTGGTTGAATAAATGAGAGAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTT 1122
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        108 TTGGTTGAATAAATGAGAGAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTT 49

Qy       1123 CAATTTCAATAAAATAAATATAAAACCATGTAACAGAA 1160
              |||||||||||||||||||||||||||| || | ||
Db          48 CAATTTCAATAAAATAAATATAAAACCATGAAAAAAAA 11


RESULT 2
BG542554
LOCUS       BG542554                 810 bp    mRNA    linear   EST 03-APR-2001
DEFINITION  602572052F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4696381 5',
            mRNA sequence.
ACCESSION   BG542554
VERSION     BG542554.1  GI:13534787
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 810)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1523  row: h  column: 14
            High quality sequence stop: 667.
FEATURES             Location/Qualifiers
     source          1. .810
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4696381"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_77"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             60.1%;  Score 719.8;  DB 12;  Length 810;
  Best Local Similarity   97.1%;  Pred. No. 3.4e-102;
  Matches  776;  Conservative    0;  Mismatches   17;  Indels    6;  Gaps    4;

Qy         78 ACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTAC 137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 ACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTAC 61

Qy        138 TGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTA 197
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Db        62 TGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTA 121

Qy       198 AGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTACAT 257
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       122 AGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTACAT 181

Qy       258 GTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTT 317
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       182 GTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTT 241

Qy       318 CAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAAT 377
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       242 CAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAAT 301

Qy       378 ACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTG 437
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       302 ACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTG 361

Qy       438 ACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCA 497
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       362 ACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCA 421

Qy       498 GGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAG 557
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       422 GGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAG 481

Qy       558 CTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACA 617
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       482 CTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACA 541

Qy       618 GTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCA 677
            |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       542 GTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGGCCCTCA 601

Qy       678 ACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGT 737
            ||||||||| |||||||||||||||| |||||||||||| | ||||||||||||||||||
Db       602 ACATTACTGT-ATAAAAGCTCCGCGTGACAAGTACTGGCTACCAATTTTTATCCCATTGT 660

Qy       738 TGGTGGTGATTCTGTTTGCTGTGGACAC--AGGATTATTTATCT-CAACTCAGCAGCAGG 794
            |||||||||||||||| |||||||||||   |||||||||||||| ||||||||||||||||
Db       661 TGGTGGTGATTCTGTTGGCTGTGGACACCAGGGATTATTTATCTCCAACTCAGCAGCAGG 720

Qy       795 TCACATTTCTC--TTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACA 852
            |||||||||||  |||| |||||  |||||| |||||||  |||||||| |||||||||
Db       721 TCACATTTCTCCTTTGACGATTAGAAGAACCCGGAAAGGGCTCAGACTCCTGAACCCAAT 780

Qy       853 TCCTAAGCCAAACCCCAAA 871
            ||||||| ||||||| |||
Db       781 TCCTAAGACAAACCCAAAA 799
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RESULT 3
CA448745/c
LOCUS       CA448745                707 bp    mRNA    linear   EST 08-NOV-2002
DEFINITION  UI-H-EI0-ayo-p-24-0-UI.s1 NCI_CGAP_EI0 Homo sapiens cDNA clone
            UI-H-EI0-ayo-p-24-0-UI 3', mRNA sequence.
ACCESSION   CA448745
VERSION     CA448745.1  GI:24813165
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 707)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            The following repetitive elements were found in this cDNA
            sequence: 93-129, >LINE2 (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .707
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-EI0-ayo-p-24-0-UI"
                     /tissue_type="Chondrosarcoma"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_EI0"
                     /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                     with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_EI0 is a cDNA library containing the following
                     tissue(s): Chondrosarcoma. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is ACACTTGCAC.
                     TAG_TISSUE=chondrosarcoma
                     TAG_LIB=UI-H-EI0
                     TAG_SEQ=ACACTTGCAC"
ORIGIN
```

Query Match 57.6%; Score 690.6; DB 14; Length 707;
Best Local Similarity 99.4%; Pred. No. 1.2e-97;
Matches 693; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy       464 GAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGAT 523
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       707 GAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGAT 648

Qy       524 GTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAC 583
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       647 GTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAC 588

Qy       584 AACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAA 643
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       587 AACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAA 528

Qy       644 GTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGT 703
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       527 GTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGT 468

Qy       704 GAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGAC 763
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       467 GAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGAC 408

Qy       764 ACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACC 823
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       407 ACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACC 348

Qy       824 AGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATAT 883
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       347 AGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATAT 288

Qy       884 AATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAA 943
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       287 AATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAA 228

Qy       944 TTGTCAAACACAGCTTGCAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATG 1003
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 TTGTCAAACACAGCTTGCAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATG 168

Qy       1004 CTTCATTAAACTGAGTGAAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACAT 1063
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 CTTCATTAAACTGAGTGAAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACAT 108

Qy       1064 TGGTTGAATAAATGAGAGAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTC 1123
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 TGGTTGAATAAATGAGAGAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTC 48

Qy       1124 AATTTCAATAAAATAAATATAAAACCATGTAACAGAA 1160
                |||||||||||||||||||||||||| || || | ||
Db         47 AATTTCAATAAAATAAATATAAAACCCTGAAAAAAAA 11


RESULT 4
CA419024/c
LOCUS       CA419024                712 bp    mRNA    linear   EST 07-NOV-2002
DEFINITION  UI-H-EZ1-bbj-e-19-0-UI.s1 NCI_CGAP_Ch2 Homo sapiens cDNA clone
            UI-H-EZ1-bbj-e-19-0-UI 3', mRNA sequence.
ACCESSION   CA419024
VERSION     CA419024.1  GI:24781675
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 712)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
            Orthoapedics
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 1-42, >(TAAAA)n#Simple_repeat (matched compliment)
            94-130, >LINE2 (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .712
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-EZ1-bbj-e-19-0-UI"
                     /tissue_type="Chondrosarcoma Grade II"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_Ch2"
                     /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                     with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_Ch2 is a normalized cDNA library containing the
                     following tissue(s): Chondrosarcoma Grade II. The library
                     was constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     TGATCACGCT.
                     TAG_TISSUE=grade-2-chondrosarcoma
                     TAG_LIB=UI-H-EZ1
                     TAG_SEQ=ATCTAATATG"
ORIGIN

  Query Match             57.5%;  Score 688.4;  DB 14;  Length 712;
  Best Local Similarity   98.7%;  Pred. No. 2.7e-97;
  Matches  692;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy        460 TGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTG 519
                ||||||||||||||||||| |||||||||||||||||||||||  |||||||||||||
Db        712 TGCTGAGGTGGTGATGGAGGNCCAGCCCCTCTTCCTCAGGTGCCATGTNTGGAGGAACTG 653

Qy        520 GGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAA 579
                |||||||||||||||||||    | ||||||||||||||||||||||||||||||||||
Db        652 GGATGTGTACAAGGTGATCTATATAANGGATGGTGAAGCTCTCAAGTACTGGTATGAGAA 593

Qy        580 CCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGG 639
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 CCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGG 533

Qy        640 CAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCC 699
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 CAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCC 473

Qy        700 GCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGT 759
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 GCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGT 413

Qy        760 GGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAG 819
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 GGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAG 353

Qy        820 AACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTG 879
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 AACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTG 293

Qy        880 ATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTAC 939
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 ATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGCTAC 233

Qy        940 TCAATTGTCAAACACAGCTTGCAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGA 999
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 TCAATTGTCAAACACAGCTTGCAATATACATAGAAACGTCTGTGCTCAAGGATTTATAGA 173

Qy       1000 AATGCTTCATTAAACTGAGTGAAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTA 1059
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 AATGCTTCATTAAACTGAGTGAAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAATTA 113

Qy       1060 ACATTGGTTGAATAAATGAGAGAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGAT 1119
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 ACATTGGTTGAATAAATGAGAGAATGAATAGATTCATTTATTAGCATTTGTAAAAGAGAT 53

Qy       1120 GTTCAATTTCAATAAAATAAATATAAAACCATGTAACAGAA 1160
                |||||||||||||||||||||||||||||||||| | ||
Db         52 GTTCAATTTCAATAAAATAAATATAAAACCATGTAAAAAAA 12


RESULT 5
AW612525/c
LOCUS       AW612525                669 bp    mRNA    linear   EST 23-MAR-2000
DEFINITION  hh03f07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2954053 3'
            similar to gb:X06948 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR
            ALPHA-SUBUNIT (HUMAN);, mRNA sequence.
ACCESSION   AW612525
VERSION     AW612525.1  GI:7317711
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
```

```
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            image.llnl.gov/image/html/iresources.shtml
            Seq primer: -40UP from Gibco
            High quality sequence stop: 438.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2954053"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Kid11"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1322376-1323911, 1456007-1456775, and
                     1500552-1502855). Subtraction by Bento Soares and M.
                     Fatima Bonaldo.  "
ORIGIN

  Query Match             53.4%;  Score 640;  DB 10;  Length 669;
  Best Local Similarity   98.2%;  Pred. No. 8.6e-90;
  Matches  657;  Conservative    0;  Mismatches   11;  Indels    1;  Gaps    1;

Qy        487 CCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAA 546
              ||||||| |||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        669 CCTCTTCTCCAGGTGCCATGGTTGCAGGAACTGGGATGTGTACAAGGTGATCTATTATAA 610

Qy        547 GGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCAC 606
              |||||||||||||||||||| |||||||||||||||||||||||||||| |||||||
Db        609 GGATGGTGAAGCTCTCAAGTGCTGGTATGAGAACCACAACATCTCCATTACATATGCCAC 550

Qy        607 AGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTC 666
              |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Db        549 AGTTGAAGACAGTGGAACCTACTACTGTACGGGCACAGTGTGGCAGCTGGAATATGAGTC 490

Qy        667 TGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAA-TTTT 725
              |||||||||||||||||||||||||| ||||| |||||||||||||||||||| ||||
Db        489 TGAGCCCCTCAACATTACTGTAATAANAGCTCTGCGTGAGAAGTACTGGCTACAATTTTT 430

Qy        726 TTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTC 785
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTC 370

Qy        786 AGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGA 845
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 AGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGA 310

Qy        846 ACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATATTTGCA 905
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 ACCCACATCTTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATATTTGCA 250

Qy        906 ACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATA 965
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 ACATTAGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATA 190

Qy        966 TACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACT 1025
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 TACATAGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACT 130

Qy       1026 GGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAATG 1085
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        129 GGTTAAGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAATG 70

Qy       1086 AATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAATATAA 1145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          69 AATAGATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAATATAA 10

Qy       1146 AACCATGTA 1154
              ||| |||||
Db          9 AACAATGTA 1


RESULT 6
BF679057
LOCUS       BF679057                834 bp    mRNA    linear   EST 21-DEC-2000
DEFINITION  602153315F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294467 5',
            mRNA sequence.
ACCESSION   BF679057
VERSION     BF679057.1  GI:11952952
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 834)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONETECH Laboratories, Inc.
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1143  row: n  column: 04
            High quality sequence stop: 621.
FEATURES             Location/Qualifiers
     source          1. .834
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4294467"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_83"
                     /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); 5' and 3' adaptors were used in cloning
                     as follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3'
                     and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.4
                     kb (range 0.5-4.0 kb).  14/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA)."
ORIGIN

  Query Match             53.2%;  Score 637;  DB 10;  Length 834;
  Best Local Similarity   95.9%;  Pred. No. 2.3e-89;
  Matches  686;  Conservative    0;  Mismatches   25;  Indels    4;  Gaps    3;

Qy          78 ACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTAC 137
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 ACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTAC 61

Qy         138 TGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTA 197
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 TGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTA 121
```

```
Qy        198 AGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTACAT 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 AGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTACAT 181

Qy        258 GTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTT 317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 GTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTT 241

Qy        318 CAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAAT 377
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 CAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAAT 301

Qy        378 ACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTG 437
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 ACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTG 361

Qy        438 ACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCA 497
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 ACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCA 421

Qy        498 GGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAG 557
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAG 481

Qy        558 CTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACA 617
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        482 CTCTCAAGTACTGGTATGAGAACCACAA-ATCTCCATTACAAATGCCACAGTTGAAGACA 540

Qy        618 GTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCA 677
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        541 GTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAG-CCCTCA 599

Qy        678 ACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATT-- 735
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |
Db        600 ACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAAATTTTTATCCCAATGG 659

Qy        736 GTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAG 790
              || |  |   |||||| ||| |  |   || | |  |||||   ||||||| |
Db        660 GTGGCGGTGAATTCTGGTTGGCGGTGGACCACGGCTTATTATCCTCACTCAGCGG 714
```

RESULT 7
BM991911/c

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LOCUS       BM991911                615 bp    mRNA    linear   EST 17-JUN-2002
DEFINITION  UI-H-DF1-auk-l-12-0-UI.s1 NCI_CGAP_DF1 Homo sapiens cDNA clone
            IMAGE:5870747 3', mRNA sequence.
ACCESSION   BM991911
VERSION     BM991911.1  GI:19711300
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 615)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             The following repetitive elements were found in this cDNA
            sequence: 90-126, >LINE2 (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .615
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5870747"
                     /tissue_type="Subchondral Bone"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_DF1"
                     /note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_DF1 is a normalized cDNA library containing the
                     following tissue(s): Subchondral Bone. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GTTAAGCGTC.
                     TAG_TISSUE=subchondral bone
                     TAG_LIB=UI-H-DF1
                     TAG_SEQ=GTTAAGCGTC"
ORIGIN
```

```
  Query Match             49.8%;  Score 596.8;  DB 12;  Length 615;
  Best Local Similarity   98.8%;  Pred. No. 4.4e-83;
  Matches  601;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        553 TGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGA 612
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        615 TGAAGCTCTCAAGTACTGGTGTGAGAACCACAACATCTCCATTACAAATGCCACAGTTGA 556

Qy        613 AGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCC 672
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 AGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCC 496

Qy        673 CCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCC 732
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        495 CCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCC 436

Qy        733 ATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCA 792
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 ATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCA 376

Qy        793 GGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACA 852
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 GGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACA 316

Qy        853 TCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATATTTGCAACATTAG 912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        315 TCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATATTTGCAACATTAG 256

Qy        913 TTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATATACATAG 972
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        255 TTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATATACATAG 196

Qy        973 AAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTAAG 1032
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        195 AAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTAAG 136

Qy       1033 TGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAATGAATAGAT 1092
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        135 TGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAATGAATAGAT 76

Qy       1093 TCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAATATAAAACCATG 1152
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db         75 TCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAATATAAACCCAAA 16

Qy       1153 TAACAGAA 1160
                |||| ||
Db         15 AAAAAAAA 8
```

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RESULT 8
BG548515
LOCUS       BG548515                840 bp    mRNA    linear   EST 04-APR-2001
DEFINITION  602576508F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4704624 5',
            mRNA sequence.
ACCESSION   BG548515
VERSION     BG548515.1  GI:13547180
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 840)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1544  row: p  column: 01
            High quality sequence stop: 590.
FEATURES             Location/Qualifiers
     source          1. .840
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4704624"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_77"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             49.0%;  Score 586.6;  DB 12;  Length 840;
  Best Local Similarity   88.2%;  Pred. No. 1.4e-81;
  Matches  735;  Conservative    0;  Mismatches   74;  Indels   24;  Gaps    8;

Qy          78 ACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTAC 137
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           2 ACAGTAAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTAC 61

Qy         138 TGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTA 197
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          62 TGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTA 121

Qy         198 AGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTACAT 257
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         122 AGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAGAATGTGACTCTTACAT 181

Qy         258 GTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTT 317
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         182 GTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTT 241

Qy         318 CAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAAT 377
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         242 CAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAAT 301

Qy         378 ACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTG 437
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         302 ACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTG 361

Qy         438 ACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCA 497
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         362 ACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCA 421

Qy         498 GGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAG 557
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         422 GGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAG 481

Qy         558 CTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT--GCCACAGTTGAAGA 615
               ||||||||||||| |||||||| |  || |||||||||| |||   |     |||||||
Db         482 CTCTCAAGTACTGTTATGAGAAACCAAAAATCTCCATTACCAATTGCCACAGTTTGAAGA 541

Qy         616 CAGTGGAACCTAC-TACTGTACGGGCAAAGTGTGGCAGCTGGAC---------TATGAGT 665
               ||||||||||||| ||||||||||||||||||||||||||||          | |||
Db         542 CAGTGGAACCTACTTACTGTACGGGCAAAGTGTGGCAGCTGGACCTATGAAGTTCTGAAG 601

Qy         666 CTGAGCCCCTCAACATTACTGTAA----TAAAAGCTCCGCGT---GAGAAGTACTGGCTA 718
               |   |   |    ||||||| |      ||| |||||| ||   || |     ||||||
Db         602 GCCCCCTTCAAACATTTACTGTTAATTTAAAATGCTCCGAGTGAAGAAAGTACTTGGCTA 661

Qy         719 CAATTTTTTATCCCATTGTTGGTGGTGATT--CTGTTTGCTGTGGACACAGGA-TTATTT 775
               ||||||| ||  |||||| ||| | ||| |  |||||||||||| || | ||| ||||||
Db         662 CAATTTTATAATCCATTGGTGGGGCTGAATCCCTGTTTGCTGTGCACCCCGGATTTATTT 721

Qy         776 ATCTCAACTCAGCA--GCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCT 833
               ||||||||||||||   |||||| ||||||||||||||   | ||  ||||  | || | |
Db         722 ATCTCAACTCAGCAAGCCAGGTCCCATTTCTCTTGAAAGATTAGGAAACCCAGGAAAGGT 781

Qy         834 TCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGATATAAT 886
               ||||| || |||||||  |||  || |||| ||| |||||||    |||| |
Db         782 TCAGAATTTTGAACCCAATTCCATAGGCAAAACCCCAAAACAATGATTATATT 834

RESULT 9
BG542157
LOCUS       BG542157                760 bp    mRNA    linear   EST 03-APR-2001
DEFINITION  602571381F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695476 5',
            mRNA sequence.
ACCESSION   BG542157
VERSION     BG542157.1  GI:13534390
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 760)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1521  row: b  column: 21
            High quality sequence stop: 751.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4695476"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_77"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
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SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 48.2%; Score 577; DB 12; Length 760;
Best Local Similarity 96.3%; Pred. No. 4.6e-80;
Matches 633; Conservative 0; Mismatches 20; Indels 4; Gaps 4;

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Qy        273 TCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATT 332
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         98 TGTTAGCAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATT 157

Qy        333 CAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACC 392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        158 CAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACC 217

Qy        393 AACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTC 452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        218 AACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTC 277

Qy        453 AGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGA 512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        278 AGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGA 337

Qy        513 GGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGT 572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        338 GGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGT 397

Qy        573 ATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACT 632
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 ATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACT 457

Qy        633 GTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAA 692
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        458 GTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAA 517

Qy        693 AAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGT 752
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        518 AAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTG- 576

Qy        753 TTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGA 812
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        577 TTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGA 636

Qy        813 TTAAGAGAACCAGGAAA-GGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAA 871
              ||||||||||||||||| |||||||||||||||||| |||||||||||| || |||
Db        637 TTAAGAGAACCAGGAAAGGGCTTCAGACTTCTGAACCCA-ATCCTAAGCCAAAACCGAAA 695

Qy        872 AACAACTGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCCAGCATCA 928
              || || |||||||||||||| ||| |||||||||   |   ||||    || || ||
Db        696 AA-AAATGATATAATTACTCCAGACATATTTGCACATTAGTTTTTCCAGCATCAGCA 751
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RESULT 10
BF678252
LOCUS BF678252 846 bp mRNA linear EST 21-DEC-2000
DEFINITION 602086161F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250222 5', mRNA sequence.
ACCESSION BF678252
VERSION BF678252.1 GI:11952147
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 846)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1071 row: j column: 15
High quality sequence stop: 609.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
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/clone="IMAGE:4250222"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_83"
/note="Organ: prostate; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.4 kb (range 0.5-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."
ORIGIN

Query Match 43.7%; Score 523.6; DB 10; Length 846;
Best Local Similarity 93.1%; Pred. No. 8.2e-72;
Matches 670; Conservative 0; Mismatches 34; Indels 16; Gaps 11;

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Qy         83 AAGCACCAGGAGTCCATGAAGAAGATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGT 142
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db          2 AAGCACCAGGAGTCCATGAAGAAGATGGCTCCTG-CATGGAATCCCCTACTCTACTGTGT 60

Qy        143 GTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTC 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTC 120

Qy        203 TCCTTGAACCCTCCATGGAATAGAATATTTAA-AGGAGAGAATGTGACTCTTACATGTAA 261
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||
Db        121 TCCTTGAACCCTCCATGGAATAGAATATTTAACAGGAGAGAATGTGACTCTTACATGTAA 180

Qy        262 TGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTTCAGA 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTTCAGA 240

Qy        322 AGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAATACAA 381
              ||||||||||||||||    |  ||||||||||||||||||||||||||||||||||||
Db        241 AGAGACAAATTCAAGTT--GAATATGTGAATGCCAAATTTGAAGACAGTGGAGAATACAA 298

Qy        382 ATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTG 441
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        299 ATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACT- 357

Qy        442 GCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTG 501
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 GCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTG 417

Qy        502 CCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCT 561
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        418 CCATGGTTGGAGGAACT-GGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCT 476

Qy        562 CAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGG 621
              |||||||| |||||||||||||||| |||||||||||||||||||| ||||||||||||
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Db        477 CAAGTACT-GTATGAGAACCACAA-ATCTCCATTACAAATGCCACAG-TGAAGACAGTGG 533

Qy        622 AACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACAT 681

Db        534 AACCTACTACTGTACGGGGCAAGTGTGGCAGCT-GACTATGAGTCTGAGCCCCTCAAAAT 592

Qy        682 TACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGT 741

Db        593 AACTGTAATAAAAGCTCGGGTGAGAAGGTACTGCTACCACTTTTTTATCCCATTGTGGGG 652

Qy        742 GGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATT 801

Db        653 GAT-----TCTGTGGCTGGGACACAGGATTA-TTATCTCAACTCAGCAGGCAGTCCCATT 706


RESULT 11
AI685796/c
LOCUS       AI685796                 540 bp    mRNA    linear   EST 27-MAY-1999
DEFINITION  tu20g08.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2251646 3'
            similar to gb:X06948 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR
            ALPHA-SUBUNIT (HUMAN);, mRNA sequence.
ACCESSION   AI685796
VERSION     AI685796.1  GI:4897090
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 540)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2251646"
                     /sex="male"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Pr28"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Plasmid DNA from the
                     normalized library NCI_CGAP_Pr22 was prepared, and ss
                     circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     985608-986759, 1101192-1101959, and 1217928-1220615).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
ORIGIN

  Query Match           41.3%;  Score 494.6;  DB 9;  Length 540;
  Best Local Similarity   95.5%;  Pred. No. 3.2e-67;
  Matches  509;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy        616 CAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCT 675

Db        533 CAATGAACCATACTACTGTACGGGCAAAGTGTGGCAGCTGGGCTAAGAGTCTGAACCCCT 474

Qy        676 CAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATT 735

Db        473 CCACAATACTGTAATATAAGCTCCGCGTAAGAAGTACTGGCTACAATTTTTTATCCCATT 414

Qy        736 GTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGT 795

Db        413 GTTGGTGGTGAATCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGT 354

Qy        796 CACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCC 855

Db        353 CACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCC 294

Qy        856 TAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATATTTGCAACATTAGTTT 915

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Qy        916 TTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATATACATAGAAA 975

Db        233 TTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACCCAGCTTGCAATATACATAGAAA 174

Qy        976 CGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTAAGTGG 1035

Db        173 CGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGGAACTAGTTAAGTGG 114

Qy       1036 CATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAATGAATAGATTCA 1095

Db        113 CATGTAATAGTAAGTGCTCGATTAACATTGGTTGAATCAATGAGAGAATGAATAGATTCA 54

Qy       1096 TTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAATATAAAAC 1148

Db         53 TTTATTAGCATTTGTAAAAGAGATGTTCACCTTCAATTAAATTAATATAAACC 1


RESULT 12
BX110472
LOCUS       BX110472                 488 bp    mRNA    linear   EST 07-FEB-2003
DEFINITION  BX110472 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGp998B235736 ;
            IMAGE:2314294, mRNA sequence.
ACCESSION   BX110472
VERSION     BX110472.1  GI:27836404
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 488)
  AUTHORS   Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
            Radelof,U., Schneider,D. and Korn,B.
  TITLE     Human UnigeneSet - RZPD3
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998B235736.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Human UnigeneSet - RZPD3 (RZPDLIB No.972)
            http://www.rzpd.de/CloneCards/cgi-
            bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
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                     /clone_lib="NCI_CGAP_Pr28"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Plasmid DNA from the
                     normalized library NCI_CGAP_Pr22 was prepared, and ss
                     circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     985608-986759, 1101192-1101959, and 1217928-1220615).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
ORIGIN

  Query Match             40.5%;  Score 484.8;  DB 13;  Length 488;
  Best Local Similarity   99.6%;  Pred. No. 1.1e-65;
  Matches  486;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        571 GTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTA 630
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTA 60

Qy        631 CTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAAT 690
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         61 CTGTACGGGCAAAGTGTGGCAGCTGGACTATTAGTCTGAGCCCCTCAACATTACTGTAAT 120

Qy        691 AAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCT 750
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCT 180

Qy        751 GTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAA 810
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAA 240

Qy        811 GATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAA 870
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAA 300

Qy        871 AAACAACTGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCCAGCATCAGC 930
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AAACAACTGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCCAGCATCAGC 360

Qy        931 AATTGCTACTCAATTGTCAAACACAGCTTGCAATATACATAGAAACGTCTGTGCTCAAGG 990
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AATTGCTACTCAATTGTCAAACACAGCTTGCAATATACATAGAAACGTCTGTGCTCAAGG 420

Qy        991 ATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTAAGTGGCATGTAATAGTAAGT 1050
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        421 ATTTATAGAAATGCTTCATTAAACTGAGTGAAACTAGTTAAGTGGCATGTAATAGTAAGT 480

Qy       1051 GCTCAATT 1058
              ||||||||
Db        481 GCTCAATT 488


RESULT 13
AI676114/c
LOCUS       AI676114                 570 bp    mRNA    linear   EST 17-DEC-1999
DEFINITION  wc05e12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314318 3'
            similar to gb:X06948 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR
            ALPHA-SUBUNIT (HUMAN);, mRNA sequence.
ACCESSION   AI676114
VERSION     AI676114.1  GI:4876594
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 570)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 625   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2314318"
                     /sex="male"
                     /dev_stage="adult"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Pr28"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Plasmid DNA from the
                     normalized library NCI_CGAP_Pr22 was prepared, and ss
                     circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     985608-986759, 1101192-1101959, and 1217928-1220615).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
ORIGIN

  Query Match             40.0%;  Score 478.8;  DB 9;  Length 570;
  Best Local Similarity   90.0%;  Pred. No. 8.6e-65;
  Matches  513;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy        571 GTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTA 630
              ||||||||| | || |    |||| | ||||||   ||   ||||||| |  |||| |
Db        570 GTATGAGAATCGCATCTGTGCCATAGCGAATGCCGAGGTGATAGACAGTAGGGCCTATTG 511

Qy        631 CTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAAT 690
              ||||  |||||||||||||||||||| |||| ||||||||||    ||||||  ||||||
Db        510 CTGTGCGGGCAAAGTGTGGCAGCTGGGCTATTAGTCTGAGCCCTCGAACATTGATGTAAT 451

Qy        691 AAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCT 750
              |||||||||||| || || |||||| ||||||||||||||||||||||||||||||||||
Db        450 AAAAGCTCCGCGTCAGGAGGACTGGCAACAATTTTTTATCCCATTGTTGGTGGTGATTCT 391

Qy        751 GTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAA 810
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 GTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAA 331

Qy        811 GATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAA 870
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        330 GATTAAGAGAACCAGGAGAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAA 271

Qy        871 AAACAACTGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCCAGCATCAGC 930
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        270 AAACAGCTGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCCAGCATCAGC 211

Qy        931 AATTGCTACTCAATTGTCAAACACAGCTTGCAATATACATAGAAACGTCTGTGCTCAAGG 990
              ||||  | |||||||| | | ||||||||||||||  ||||||||||||||||||||
Db        210 GATTGTGGTCGAGTTGTCAAGCGCGGCTTGCAATATACATAACAACGTCTGTGCTCAAGG 151

Qy        991 ATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTAAGTGGCATGTAATAGTAAGT 1050
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
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Db        150 ATTTATAGAAATGCTTCATTAAACTGAGTGAAACTAGTTAAGTGGCATGTAATAGTAAGT 91

Qy       1051 GCTCAATTAACATTGGTTGAATAAATGAGAGAATGAATAGATTCATTTATTAGCATTTGT 1110
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         90 GCTCAATTAACATTGGTTGAATGAATGAGAGAATGAATAGATTCATTTATTAGCATTTGT 31

Qy       1111 AAAAGAGATGTTCAATTTCAATAAAATAAA 1140
              |||||||  | |||||||||||| |   ||
Db         30 AAAAGAGCCGCTCAATTTCAATAGATAGAA 1
```

RESULT 14
BQ005218/c

LOCUS	BQ005218	478 bp	mRNA	linear	EST 26-MAR-2002

DEFINITION UI-H-EI1-azg-h-15-0-UI.s1 NCI_CGAP_EI1 Homo sapiens cDNA clone IMAGE:5848382 3', mRNA sequence.
ACCESSION BQ005218
VERSION BQ005218.1 GI:19730118
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 478)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
The following repetitive elements were found in this cDNA sequence: 97-133, >LINE2 (matched compliment)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES Location/Qualifiers
source 1. .478
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5848382"
/tissue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_EI1"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_EI1 is a normalized cDNA library containing the following tissue(s): Chondrosarcoma. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is ACACTTGCAC.
TAG_TISSUE=chondrosarcoma
TAG_LIB=UI-H-EI1
TAG_SEQ=ACACTTGCAC"

ORIGIN

Query Match 38.7%; Score 464; DB 12; Length 478;
Best Local Similarity 100.0%; Pred. No. 1.8e-62;
Matches 464; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        697 TCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGC 756
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 TCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGC 419

Qy        757 TGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAA 816
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 TGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAA 359

Qy        817 GAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAA 876
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 GAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAA 299

Qy        877 CTGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGC 936
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 CTGATATAATTACTCAAGAAATATTTGCAACATTAGTTTTTTTCCAGCATCAGCAATTGC 239

Qy        937 TACTCAATTGTCAAACACAGCTTGCAATATACATAGAAACGTCTGTGCTCAAGGATTTAT 996
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 TACTCAATTGTCAAACACAGCTTGCAATATACATAGAAACGTCTGTGCTCAAGGATTTAT 179

Qy        997 AGAAATGCTTCATTAAACTGAGTGAAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAA 1056
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 AGAAATGCTTCATTAAACTGAGTGAAACTGGTTAAGTGGCATGTAATAGTAAGTGCTCAA 119

Qy       1057 TTAACATTGGTTGAATAAATGAGAGAATGAATAGATTCATTTATTAGCATTTGTAAAAGA 1116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        118 TTAACATTGGTTGAATAAATGAGAGAATGAATAGATTCATTTATTAGCATTTGTAAAAGA 59

Qy       1117 GATGTTCAATTTCAATAAAATAAATATAAAACCATGTAACAGAA 1160
              ||||||||||||||||||||||||||||||||||||||||||||
Db         58 GATGTTCAATTTCAATAAAATAAATATAAAACCATGTAACAGAA 15
```

RESULT 15
BF593204/c

LOCUS	BF593204	479 bp	mRNA	linear	EST 12-DEC-2000

DEFINITION 7o50c04.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:3577351 3' similar to SW:FCEA_HUMAN P12319 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR ALPHA-SUBUNIT PRECURSOR ;, mRNA sequence.
ACCESSION BF593204
VERSION BF593204.1 GI:11685528
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 479)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 325.

FEATURES Location/Qualifiers
source 1. .479
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3577351"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Kid11"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI;

Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1322376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 38.0%; Score 455; DB 10; Length 479;
Best Local Similarity 96.9%; Pred. No. 4.6e-61;
Matches 464; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

```
Qy       671 CCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATC 730
            ||||||||||||| ||||| |||     |   || ||| |||| || |||| ||||| |||
Db       479 CCCCTCAACATTATTGTAAAAAAGCTCCGCGGTAAGAGGTACGGGATACATTTTTTAATC 420

Qy       731 CCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAG 790
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       419 CCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAG 360

Qy       791 CAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCA 850
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       359 CAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCA 300

Qy       851 CATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATATTTGCAACATT 910
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       299 CATCCTAAGCCAAACCCCAAAAACAACTGATATAATTACTCAAGAAATATTTGCAACATT 240

Qy       911 AGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATATACAT 970
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       239 AGTTTTTTTCCAGCATCAGCAATTGCTACTCAATTGTCAAACACAGCTTGCAATATACAT 180

Qy       971 AGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTA 1030
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       179 AGAAACGTCTGTGCTCAAGGATTTATAGAAATGCTTCATTAAACTGAGTGAAACTGGTTA 120

Qy      1031 AGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAATGAATAG 1090
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       119 AGTGGCATGTAATAGTAAGTGCTCAATTAACATTGGTTGAATAAATGAGAGAATGAATAG 60

Qy      1091 ATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAATATAAAACC 1149
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         59 ATTCATTTATTAGCATTTGTAAAAGAGATGTTCAATTTCAATAAAATAAATATAAAACC 1
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Search completed: October 10, 2004, 19:44:35
Job time : 4048.38 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:39 ; Search time 8.68648 Seconds
(without alignments)
1540.558 Million cell updates/sec

Title: US-10-763-400-2
Perfect score: 1390
Sequence: 1 MAPAMESPTLLCVALLFFAP.....RTRKGFRLLNPHPKPNPKNN 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1390	100.0	257	1	FCEA_HUMAN	P12319 homo sapien
2	626.5	45.1	250	1	FCEA_MOUSE	P20489 mus musculu
3	597.5	43.0	245	1	FCE1_RAT	P12371 rattus norv
4	419	30.1	257	1	FCG3_PIG	Q28942 sus scrofa
5	418	30.1	254	1	FC3A_HUMAN	P08637 homo sapien
6	417	30.0	250	1	FCG3_BOVIN	P79107 bos taurus
7	406	29.2	233	1	FC3B_HUMAN	O75015 homo sapien
8	405	29.1	296	1	FCG2_BOVIN	Q28110 bos taurus
9	401.5	28.9	261	1	FCG3_MOUSE	P08508 mus musculu
10	400	28.8	267	1	FCG3_RAT	P27645 rattus norv
11	395	28.4	341	1	FCG2_CAVPO	Q60513 cavia porce
12	379	27.3	374	1	FCG1_HUMAN	P12314 homo sapien
13	379	27.3	404	1	FCG1_MOUSE	P26151 mus musculu
14	371.5	26.7	310	1	FCGB_HUMAN	P31994 homo sapien
15	371.5	26.7	323	1	FCGC_HUMAN	P31995 homo sapien
16	368	26.5	285	1	FCG2_RAT	Q63203 rattus norv
17	367	26.4	330	1	FCG2_MOUSE	P08101 mus musculu
18	351	25.3	316	1	FCGA_PANTR	Q8spv8 pan troglod
19	348	25.0	157	1	FCE2_RAT	P12840 rattus norv
20	347	25.0	317	1	FCGA_HUMAN	P12318 homo sapien
21	175.5	12.6	1709	1	SN_HUMAN	Q9bzz2 homo sapien
22	166	11.9	1694	1	SN_MOUSE	Q62230 mus musculu
23	154	11.1	422	1	K3L1_RAT	P83556 rattus norv
24	144	10.4	432	1	K3L1_MOUSE	P83555 mus musculu
25	137.5	9.9	521	1	CEA1_MOUSE	P31809 mus musculu
26	137.5	9.9	837	1	NCM2_MOUSE	O35136 mus musculu
27	136.5	9.8	519	1	ECTO_RAT	P16573 rattus norv
28	129.5	9.3	1302	1	NRG_DROME	P20241 drosophila
29	128.5	9.2	344	1	CEA6_HUMAN	P40199 homo sapien
30	126	9.1	1240	1	NFAS_HUMAN	O94856 homo sapien
31	125.5	9.0	978	1	KFMS_RAT	Q00495 rattus norv
32	125	9.0	458	1	CD4_MACNE	Q08340 macaca neme
33	124.5	9.0	977	1	KFMS_MOUSE	P09581 mus musculu
34	123	8.8	1240	1	NFAS_MOUSE	Q810u3 mus musculu
35	123	8.8	1240	1	NFAS_RAT	P97685 rattus norv
36	122	8.8	458	1	CD4_CERAE	Q08338 cercopithec
37	121.5	8.7	739	1	VCAM_RAT	P29534 rattus norv
38	120	8.6	458	1	CD4_MACFU	P79184 macaca fusc
39	120	8.6	702	1	CEA5_HUMAN	P06731 homo sapien
40	120	8.6	837	1	NCM2_HUMAN	O15394 homo sapien
41	120	8.6	847	1	CD22_HUMAN	P20273 homo sapien
42	120	8.6	862	1	CD22_MOUSE	P35329 mus musculu
43	120	8.6	6632	1	UN89_CAEEL	O01761 caenorhabdi
44	119	8.6	458	1	CD4_MACMU	P16003 macaca mula
45	119	8.6	739	1	VCAM_HUMAN	P19320 homo sapien

ALIGNMENTS

RESULT 1
FCEA_HUMAN
ID FCEA_HUMAN STANDARD; PRT; 257 AA.
AC P12319;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor
DE (FcERI) (IgE Fc receptor, alpha-subunit) (Fc-epsilon RI-alpha).
GN FCER1A OR FCE1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88233953; PubMed=2967464;
RA Kochan J., Pettine L.F., Hakimi J., Kishi K., Kinet J.-P.;
RT "Isolation of the gene coding for the alpha subunit of the human high
RT affinity IgE receptor.";
RL Nucleic Acids Res. 16:3584-3584(1988).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Mast cells;
RX MEDLINE=88158102; PubMed=2964640;
RA Shimizu A., Tepler I., Benfey P.N., Berenstein E.H., Siraganian R.P.,
RA Leder P.;
RT "Human and rat mast cell high-affinity immunoglobulin E receptors:
RT characterization of putative alpha-chain gene products.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).
RN [3]
RP 3D-STRUCTURE MODELING OF 26-197.
RX MEDLINE=93113350; PubMed=1472946;
RA Padlan E.A., Helm B.A.;
RT "A modeling study of the alpha-subunit of human high-affinity
RT receptor for immunoglobulin-E.";
RL Receptor 2:129-144(1992).
CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH
CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
CC ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.
CC -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO
CC DISULFIDE LINKED GAMMA CHAINS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like domains.
CC ----------

CC ----------

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DR   EMBL; X06948; CAA30025.1; -.
DR   EMBL; J03605; AAA36204.1; -.
DR   EMBL; A21606; CAA01564.1; -.
DR   PIR; S00682; S00682.
DR   PDB; 1ALS; 27-FEB-95.
DR   PDB; 1ALT; 27-FEB-95.
DR   PDB; 1F2Q; 08-JUN-00.
DR   PDB; 1J86; 29-AUG-01.
DR   PDB; 1J87; 29-AUG-01.
DR   PDB; 1J88; 29-AUG-01.
DR   PDB; 1J89; 05-SEP-01.
DR   Genew; HGNC:3609; FCER1A.
DR   MIM; 147140; -.
DR   GO; GO:0005887; C:integral to plasma membrane; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   IgE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Immunoglobulin domain; Repeat; 3D-structure.
FT   SIGNAL       1    25
FT   CHAIN       26   257       HIGH AFFINITY IMMUNOGLOBULIN EPSILON
FT                               RECEPTOR ALPHA-SUBUNIT.
FT   DOMAIN      26   205       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   206   224       POTENTIAL.
FT   DOMAIN     225   257       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      30   110       IG-LIKE 1.
FT   DOMAIN     111   193       IG-LIKE 2.
FT   DISULFID    51    93       BY SIMILARITY.
FT   DISULFID   132   176       BY SIMILARITY.
FT   CARBOHYD    46    46       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    67    67       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    75    75       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    99    99       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   160   160       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   165   165       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   191   191       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   STRAND      31    35
FT   HELIX       39    42
FT   TURN        43    43
FT   STRAND      48    54
FT   STRAND      61    66
FT   TURN        67    68
FT   STRAND      69    71
FT   STRAND      74    74
FT   TURN        75    76
FT   STRAND      77    79
FT   HELIX       82    87
FT   STRAND      91    96
FT   HELIX       98   100
FT   TURN       101   101
FT   STRAND     104   107
FT   STRAND     114   116
FT   HELIX      120   124
FT   STRAND     128   133
FT   STRAND     143   145
FT   HELIX      146   148
FT   TURN       149   149
FT   STRAND     150   150
FT   TURN       152   153
FT   STRAND     154   155
FT   TURN       156   159
FT   STRAND     160   163
FT   HELIX      165   170
FT   STRAND     175   178
FT   STRAND     181   182
FT   TURN       183   185
FT   STRAND     186   187
FT   STRAND     190   193
SQ   SEQUENCE   257 AA;  29596 MW;  F183BB2357DDAD58 CRC64;

  Query Match             100.0%;  Score 1390;  DB 1;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 1.9e-107;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||||||||||
Db        241 KGFRLLNPHPKPNPKNN 257


RESULT 2
FCEA_MOUSE
ID   FCEA_MOUSE     STANDARD;      PRT;   250 AA.
AC   P20489;
DT   01-FEB-1991 (Rel. 17, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   High affinity immunoglobulin epsilon receptor alpha-subunit precursor
DE   (FCERI) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha).
GN   FCER1A OR FCE1A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89359361; PubMed=2527850;
RA   Ra C., Jouvin M.H.E., Kinet J.-P.;
RT   "Complete structure of the mouse mast cell receptor for IgE (Fc
RT   epsilon RI) and surface expression of chimeric receptors
RT   (rat-mouse-human) on transfected cells.";
RL   J. Biol. Chem. 264:15323-15327(1989).
CC   -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH
CC       AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
CC       RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
CC       ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
CC       RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
CC       ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.
CC   -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO
CC       DISULFIDE LINKED GAMMA CHAINS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like domains.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; J05018; AAA37600.1; -.
DR   PIR; A34342; A34342.
DR   HSSP; P12319; 1ALS.
DR   MGD; MGI:95494; Fcer1a.
DR   GO; GO:0007165; P:signal transduction; IDA.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   Pfam; PF00047; ig; 2.
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DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   IgE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Immunoglobulin domain; Repeat.
FT   SIGNAL        1     23
FT   CHAIN        24    250       HIGH AFFINITY IMMUNOGLOBULIN EPSILON
FT                                 RECEPTOR ALPHA-SUBUNIT.
FT   DOMAIN       24    204       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    205    223       POTENTIAL.
FT   DOMAIN      224    250       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       28    104       IG-LIKE 1.
FT   DOMAIN      114    181       IG-LIKE 2.
FT   DISULFID     49     92       BY SIMILARITY.
FT   DISULFID    131    174       BY SIMILARITY.
FT   CARBOHYD     58     58       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     66     66       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     73     73       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    106    106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    152    152       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    167    167       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   250 AA;  28672 MW;  2575D1BFB4DC0C4E CRC64;

  Query Match             45.1%;  Score 626.5;  DB 1;  Length 250;
  Best Local Similarity   51.9%;  Pred. No. 1.4e-44;
  Matches  121;  Conservative   46;  Mismatches   63;  Indels    3;  Gaps    3;

Qy         11 LCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEV-SSTKWFHNGS 69
              ||:|||| : | :|   :|  ::|:||| ||| || |||:| |||  :: |:||| |||:
Db          9 LCLALLFMSLDVILTATEKSVLTLDPPWIRIFTGEKVTLSCYGNNHLQMNSTTKWIHNGT 68

Qy         70 LSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLF 129
              :|  :| | ||:|  :|||:| || | : :|:|||| |  ||||| ||:::
Db         69 VSEVNSSHLVIVSATVQDSGKYICQKQGLFKSKPVYLNVTQDWLLLQTSADMILVHGSFD 128

Qy        130 LRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEP 189
              :|||||:||:| |||||::  |  | ||:  :||  ||: |||||:| | : |::|||:
Db        129 IRCHGWKNWNVRKVIYYRNDHAFNYSYES-PVSIREATLNDSGTYHCKGYLRQVEYESDK 187

Qy        190 LNITVIKAPREK-YWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRK 241
                | |:|| : | ||||   |||| |||||||||| :||::|   :|:|::| |
Db        188 FRIAVVKAYKCKYYWLQLIPPLLVAILFAVDTGLLLSTEEQFKSVLEIQKTGK 240


RESULT 3
FCE1_RAT
ID   FCE1_RAT       STANDARD;      PRT;   245 AA.
AC   P12371;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   High affinity immunoglobulin epsilon receptor alpha-subunit precursor
DE   (FCERI) (IGE FC receptor, alpha-subunit) (FC-epsilon RI-alpha).
GN   FCER1A OR FCE1A.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88024987; PubMed=2959318;
RA   Kinet J.-P., Metzger H., Hakimi J., Kochan J.;
RT   "A cDNA presumptively coding for the alpha subunit of the receptor
RT   with high affinity for immunoglobulin E.";
RL   Biochemistry 26:4605-4610(1987).
RN   [2]
RP   REVISIONS.
RA   Kochan J.;
RL   Submitted (MAR-1988) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Mast cells;
RX   MEDLINE=88158102; PubMed=2964640;
RA   Shimizu A., Tepler I., Benfey P.N., Berenstein E.H., Siraganian R.P.,
RA   Leder P.;
RT   "Human and rat mast cell high-affinity immunoglobulin E receptors:
RT   characterization of putative alpha-chain gene products.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).
RN   [4]
RP   SEQUENCE OF 21-245 FROM N.A.
RX   MEDLINE=88289772; PubMed=2969594;
RA   Liu F.-T., Albrandt K., Robertson M.W.;
RT   "cDNA heterogeneity suggests structural variants related to the high-
RT   affinity IgE receptor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 85:5639-5643(1988).
CC   -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS EPSILON. HIGH
CC       AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
CC       RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
CC       ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
CC       RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
CC       ALSO INDUCES THE SECRETION OF IMPORTANT LYMPHOKINES.
CC   -!- SUBUNIT: TETRAMER OF AN ALPHA CHAIN, A BETA CHAIN, AND TWO
CC       DISULFIDE LINKED GAMMA CHAINS.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like domains.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M17153; AAA42045.1; -.
DR   EMBL; J03606; AAA41582.1; -.
DR   EMBL; M21622; AAA41146.1; -.
DR   PIR; C31327; A30154.
DR   HSSP; P12319; 1ALS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   IgE-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Immunoglobulin domain; Repeat.
FT   SIGNAL        1     23
FT   CHAIN        24    245       HIGH AFFINITY IMMUNOGLOBULIN EPSILON
FT                                 RECEPTOR ALPHA-SUBUNIT.
FT   DOMAIN       24    204       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    205    223       POTENTIAL.
FT   DOMAIN      224    245       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       28    103       IG-LIKE 1.
FT   DOMAIN      113    181       IG-LIKE 2.
FT   DISULFID     49     91       BY SIMILARITY.
FT   DISULFID    130    174       BY SIMILARITY.
FT   CARBOHYD     52     52       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     53     53       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     58     58       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     65     65       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    123    123       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    158    158       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    167    167       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   245 AA;  27793 MW;  A0E67DD363B72197 CRC64;

  Query Match             43.0%;  Score 597.5;  DB 1;  Length 245;
  Best Local Similarity   49.8%;  Pred. No. 3.2e-42;
  Matches  116;  Conservative   43;  Mismatches   73;  Indels    1;  Gaps    1;

Qy         11 LCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSL 70
              ||:||:  :   :|   ||  |||:||| ||  |: ||| |||||  :::|||| || |:
Db          9 LCLALVLISLGVMLTATQKSVVSLDPPWIRILTGDKVTLICNGNNSSQMNSTKWIHNDSI 68

Qy         71 SEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFL 130
              |   :|   ||:|  :|||:| || |   :|:|||| |  :|||||:||:||::     :
Db         69 SNVKSSHWVIVSATIQDSGKYICQKQGFYKSKPVYLNVMQEWLLLQSSADVVLDNGSFDI 128
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Qy        131 RCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPL 190
              ||  |: | |:|||||||  | || |:::|||  ||  |||:|:||| : ::: :|:
Db        129 RCRSWKKWKVHKVIYYKDDIAFKYSYDSNNISIRKATFNDSGSYHCTGYLNKVECKSDKF 188

Qy        191 NITVIKAPREKY-WLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKG 242
              :| |:|    :| |||   | | ||||||||||: || :|   :|||::| ||
Db        189 SIAVVKDYTIEYRWLQLIFPSLAVILFAVDTGLWFSTHKQFESILKIQKTGKG 241


RESULT 4
FCG3_PIG
ID   FCG3_PIG       STANDARD;      PRT;   257 AA.
AC   Q28942; Q28940; Q28941;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Low affinity immunoglobulin gamma Fc region receptor III precursor
DE   (IgG Fc receptor III) (Fc-gamma RIII) (FcRIII) (Cytolytic trigger
DE   molecule G7).
GN   FCGR3.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 27-47; 92-107 AND 179-188.
RC   STRAIN=Minnesota miniature swine;
RX   MEDLINE=94358430; PubMed=8077673;
RA   Halloran P.J., Sweeney S.E., Strohmeier C.M., Kim Y.B.;
RT   "Molecular cloning and identification of the porcine cytolytic
RT   trigger molecule G7 as a Fc gamma RIII alpha (CD16) homologue.";
RL   J. Immunol. 153:2631-2641(1994).
CC   -!- FUNCTION: Receptor for the Fc region of complexed immunoglobulins
CC       gamma. Low affinity receptor.
CC   -!- SUBUNIT: FORMS A COMPLEX WITH NK-E.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: FOUND IN POLYMORPHONUCLEAR CELLS (PMN), PBMC,
CC       MACROPHAGES, SPLEEN, AND AT LOW LEVELS IN LYMPH NODES BUT NOT IN
CC       THYMUS OR LIVER.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U08993; AAA57190.1; -.
DR   EMBL; U08991; AAA57188.1; -.
DR   EMBL; U08992; AAA57189.1; -.
DR   HSSP; P12319; 1ALS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Immunoglobulin domain; Repeat.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    257       LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
FT                                 REGION RECEPTOR III.
FT   DOMAIN       20    209       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    210    230       POTENTIAL.
FT   DOMAIN      231    257       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       25    104       IG-LIKE C2-TYPE 1.
FT   DOMAIN      108    190       IG-LIKE C2-TYPE 2.
FT   DISULFID     48     90       BY SIMILARITY.
FT   DISULFID    129    173       BY SIMILARITY.
FT   CARBOHYD     64     64       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    134    134       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    162    162       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    181    181       N-LINKED (GLCNAC. . .) (IN CLONE 334.8)
FT                                 (POTENTIAL).
FT   VARIANT      55     55       R -> G (IN CLONE 284.4).
FT   VARIANT     149    149       K -> M (IN CLONE 334.8).
FT   VARIANT     181    181       D -> N (IN CLONE 334.8).
FT   VARIANT     186    186       P -> A (IN CLONE 334.8).
SQ   SEQUENCE   257 AA;  29062 MW;  1D038CC1552B97CB CRC64;

  Query Match             30.1%;  Score 419;  DB 1;  Length 257;
  Best Local Similarity   38.8%;  Pred. No. 1.7e-27;
  Matches   94;  Conservative   41;  Mismatches   91;  Indels   16;  Gaps    3;

Qy          7 SPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFH 66
              ||| |   ||   |     | |  | |:|||:|: : ::||| | |       ||:|
Db          6 SPTAL--LLLVSVPGTHAEDPPKSVVILDPPWDRLLEKDSVTLKCQGAYPPRDDSTEWRW 63

Qy         67 NGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQ 126
              ||:|     || :| :|   :|||| |:     :|:|: |||:  ||||||   || ||:
Db         64 NGTLISNKASSYSITDATVGNSGEYTCKTGLSAQSDPLRLEVYKGWLLLQAPRWVVQEGE 123

Qy        127 PLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYE 186
              : |||| |:|  : || |:::|   |: ::|     | |||::| |:|:| | :   |
Db        124 SIRLRCHTWKNITIQKVQYFQNGMGKKFSHQNFEYHIPNATLKDGGSYFCRGIIKNYDLS 183

Qy        187 SEPLNITVIKAPREKYWLQFFIP-------LLVVILFAVDTGLFISTQQQVTFLLKIKRT 239
              |||: :||  :       | ||:|       |::  |||||||: | :       |: |:
Db        184 SEPVKVTVQGSKSPSPILSFFLPWHQIIFCLVMGFLFAVDTGLYFSVR-------KVLRS 236

Qy        240 RK 241
              ||
Db        237 SK 238


RESULT 5
FC3A_HUMAN
ID   FC3A_HUMAN     STANDARD;      PRT;   254 AA.
AC   P08637;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1990 (Rel. 15, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Low affinity immunoglobulin gamma Fc region receptor III-A precursor
DE   (IgG FC receptor III-2) (Fc-gamma RIII-alpha) (Fc-gamma RIIIA)
DE   (FcRIIIA) (Fc-gamma RIII) (FcRIII) (CD16-A) (FcR-10).
GN   FCGR3A OR FCG3 OR FCGR3 OR IGFR3 OR CD16A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89328325; PubMed=2526846;
RA   Ravetch J.V., Perussia B.;
RT   "Alternative membrane forms of Fc gamma RIII(CD16) on human natural
RT   killer cells and neutrophils. Cell type-specific expression of two
RT   genes that differ in single nucleotide substitutions.";
RL   J. Exp. Med. 170:481-497(1989).
RN   [2]
RP   SEQUENCE OF 1-39 FROM N.A.
RC   TISSUE=Placenta;
RX   MEDLINE=95138131; PubMed=7836402;
RA   Gessner J.E., Grussenmeyer T., Kolanus W., Schmidt R.E.;
RT   "The human low affinity immunoglobulin G Fc receptor III-A and III-B
RT   genes. Molecular characterization of the promoter regions.";
RL   J. Biol. Chem. 270:1350-1361(1995).
RN   [3]
RP   VARIANTS ARG-66 AND HIS-66.
RX   MEDLINE=96183251; PubMed=8609432;
RA   de Haas M., Koene H.R., Kleijer M., de Vries E., Simsek S.,
RA   van Tol M.J.D., Roos D., von dem Borne A.E.G.K.;
RT   "A triallelic Fc gamma receptor type IIIA polymorphism influences the
RT   binding of human IgG by NK cell Fc gamma RIIIa.";
RL   J. Immunol. 156:3948-3955(1996).
RN   [4]
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```
RP   VARIANT VAL-157.
RX   MEDLINE=97385047; PubMed=9242542;
RA   Koene H.R., Kleijer M., Algra J., Roos D., von dem Borne A.E.G.K.,
RA   de Haas M.;
RT   "Fc gammaRIIIa-158V/F polymorphism influences the binding of IgG by
RT   natural killer cell Fc gammaRIIIa, independently of the Fc
RT   gammaRIIIa-48L/R/H phenotype.";
RL   Blood 90:1109-1114(1997).
RN   [5]
RP   VARIANT VAL-176.
RX   MEDLINE=97426467; PubMed=9276722;
RA   Wu J., Edberg J.C., Redecha P.B., Bansal V., Guyre P.M., Coleman K.,
RA   Salmon J.E., Kimberly R.P.;
RT   "A novel polymorphism of FcgammaRIIIa (CD16) alters receptor function
RT   and predisposes to autoimmune disease.";
RL   J. Clin. Invest. 100:1059-1070(1997).
CC   -!- FUNCTION: RECEPTOR FOR THE FC REGION OF IGG. BINDS COMPLEXED OR
CC       AGGREGATED IGG AND ALSO MONOMERIC IGG. MEDIATES ANTIBODY-DEPENDENT
CC       CELLULAR CYTOTOXICITY (ADCC) AND OTHER ANTIBODY-DEPENDENT
CC       RESPONSES, SUCH AS PHAGOCYTOSIS.
CC   -!- SUBUNIT: EXISTS AS A HETERO-OLIGOMERIC RECEPTOR COMPLEX WITH FC
CC       EPSILON RECEPTOR I GAMMA SUBUNIT AND / OR THE CD3 ZETA SUBUNIT.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential). Exists
CC       also as a soluble receptor.
CC   -!- TISSUE SPECIFICITY: Expressed on natural killer cells,
CC       macrophages, subpopulation of T cells, immature thymocytes and
CC       placental trophoblasts.
CC   -!- PTM: Glycosylated. Contains high mannose-and complex-type
CC       oligosaccharides.
CC   -!- PTM: The soluble form is produced by a proteolytic cleavage.
CC   -!- POLYMORPHISM: Isoform Val-157 shows a higher binding capacity of
CC       IgG1, IgG3 and IgG4 compared with isoform Phe-157. Alleles Leu-66
CC       and Phe-157, and alleles His-66 / Arg-66 and Val-157 are in
CC       linkage desequilibrium.
CC   -!- MISCELLANEOUS: ENCODED BY ONE OF TWO NEARLY INDENTICAL GENES:
CC       FCGR3A (SHOWN HERE) AND FCGR3B WHICH ARE EXPRESSED IN A TISSUE-
CC       SPECIFIC MANNER. THE PHE-203 IN III-A DETERMINES THE TRANSMEMBRANE
CC       DOMAINS WHEREAS THE SER-203 IN III-B DETERMINES THE GPI-ANCHORING.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD16A entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd16a.htm".
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X52645; CAA36870.1; -.
DR   EMBL; Z46222; CAA86295.1; -.
DR   PIR; JL0107; JL0107.
DR   HSSP; P12319; 1ALS.
DR   Genew; HGNC:3619; FCGR3A.
DR   MIM; 146740; -.
DR   GO; GO:0005886; C:plasma membrane; TAS.
DR   GO; GO:0006955; P:immune response; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Immunoglobulin domain; Repeat; Multigene family; Polymorphism.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    254       LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
FT                                REGION RECEPTOR III-A.
FT   DOMAIN       17    208       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    209    229       POTENTIAL.
FT   DOMAIN      230    254       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       24    105       IG-LIKE C2-TYPE 1.
FT   DOMAIN      107    189       IG-LIKE C2-TYPE 2.
FT   DISULFID     47     89       BY SIMILARITY.
FT   DISULFID    128    172       BY SIMILARITY.
FT   CARBOHYD     56     56       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     63     63       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     92     92       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    187    187       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      66     66       L -> R.
FT                                /FTId=VAR_008799.
FT   VARIANT      66     66       L -> H.
FT                                /FTId=VAR_008800.
FT   VARIANT     157    157       F -> V.
FT                                /FTId=VAR_008801.
FT   VARIANT     176    176       F -> V (in dbSNP:396991).
FT                                /FTId=VAR_003960.
SQ   SEQUENCE   254 AA;  29089 MW;  D38D178D32C67337 CRC64;

  Query Match             30.1%;  Score 418;  DB 1;  Length 254;
  Best Local Similarity   40.9%;  Pred. No. 2e-27;
  Matches   94;  Conservative   34;  Mismatches   92;  Indels   10;  Gaps    3;

Qy         10 LLCVALLFFAPDGVLAVPQKPK--VSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHN 67
              ||  |||     | :    ||  | | | | | : : ::||| | |     | :||:||||
Db          5 LLPTALLLLVSAG-MRTEDLPKAVVFLEPQWYRVLEKDSVTLKCQGAYSPEDNSTQWFHN 63

Qy         68 GSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQP 127
              ||      ||  |  |  :|||||:||      |:|| |||   ||||||   |  |  |
Db         64 ESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLQAPRWVFKEEDP 123

Qy        128 LFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYES 187
              : |||| |:|  ::|| | ::|:  ||:: | :  |  ||::|||:|:| |     :  |
Db        124 IHLRCHSWKNTALHKVTYLQNGKGRKYFHHNSDFYIPKATLKDSGSYFCRGLFGSKNVSS 183

Qy        188 EPLNITVIKAPREKYWLQFFIP-------LLVVILFAVDTGLFISTQQQV 230
              | :|||: :          || |       |::|:||||||||: | :  :
Db        184 ETVNITITQGLAVSTISSFFPPGYQVSFCLVMVLLFAVDTGLYFSVKTNI 233


RESULT 6
FCG3_BOVIN
ID   FCG3_BOVIN     STANDARD;      PRT;   250 AA.
AC   P79107;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Low affinity immunoglobulin gamma Fc region receptor III precursor
DE   (IgG Fc receptor III) (Fc-gamma RIII) (FcRIII).
GN   FCGR3 OR FCGRIII.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Lymph node;
RX   MEDLINE=97246739; PubMed=9089104;
RA   Collins R.A., Gelder K.I., Howard C.J.;
RT   "Nucleotide sequence of cattle FcGRIII: its identification in
RT   gammadelta T cells.";
RL   Immunogenetics 45:440-443(1997).
CC   -!- FUNCTION: IS A RECEPTOR FOR THE FC REGION OF IGG. BINDS COMPLEXED
CC       OR AGGREGATED IGG AND ALSO MONOMERIC IGG. ALSO MEDIATES ANTIBODY-
CC       DEPENDENT CELLULAR TOXICITY (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN GAMMA-DELTA T CELLS.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   -!- CAUTION: IT IS NOT SURE IF THE VARIANTS ARE DUE TO DIFFERENT
CC       ALLELES OR TO THE EXISTENCE OF AT LEAST TWO GENES.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; X99695; CAA68026.1; -.
DR   HSSP; P12319; 1ALS.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Immunoglobulin domain; Repeat; Polymorphism.
FT   SIGNAL        1     16       POTENTIAL.
FT   CHAIN        17    250       LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
FT                                 REGION RECEPTOR III.
FT   DOMAIN       17    208       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    209    225       POTENTIAL.
FT   DOMAIN      226    250       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       23    105       IG-LIKE C2-TYPE 1.
FT   DOMAIN       99    189       IG-LIKE C2-TYPE 2.
FT   DISULFID     47     89       BY SIMILARITY.
FT   DISULFID    128    172       BY SIMILARITY.
FT   CARBOHYD     56     56       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     63     63       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT      11     11       P -> L.
FT   VARIANT      12     12       V -> L.
FT   VARIANT      46     46       K -> R.
FT   VARIANT     107    107       G -> D.
FT   VARIANT     114    114       A -> V.
FT   VARIANT     229    229       V -> I.
SQ   SEQUENCE   250 AA;  28050 MW;  DE625139E889E207 CRC64;

  Query Match             30.0%;  Score 417;  DB 1;  Length 250;
  Best Local Similarity   38.2%;  Pred. No. 2.4e-27;
  Matches   91;  Conservative   38;  Mismatches   93;  Indels   16;  Gaps    3;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              : |    | |:       : |   | | |  | |:| || :   : ||| | |:   | :
Db          4 LLPPAALPVLV-------SADTQTADPSKAVVLLDPQWNHVLTNDRVTLKCQGDYPVEDN 56

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||:|||:|      |  | : | :|||||||      |:|| |||   ||||| :
Db         57 STKWWHNGTLISSQTPSYFIADVKVQDSGEYKCQTGLSAPSDPVKLEVHVGWLLLQVAQR 116

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||  |:|: |:|| |:   | || |:::|   || : | :  |  | :| ||:|:| | :
Db        117 VVNVGKPIRLKCHSWKKTPVAKVQYFRNGRGKKYSHGNSDFHIPEAKLEHSGSYFCRGII 176

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIP--------LLVVILFAVDTGLFISTQQQV 230
                :  || : ||| :||     :  | |         |:: :||||||: | :: :
Db        177 GSKNESSESVQITV-QAPETLQTVSSFFPPWHQITFCLVMGVLFAVDTGLYFSVRRHL 233


RESULT 7
FC3B_HUMAN
ID   FC3B_HUMAN     STANDARD;      PRT;   233 AA.
AC   O75015;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Low affinity immunoglobulin gamma Fc region receptor III-B precursor
DE   (IgG Fc receptor III-1) (Fc-gamma RIII-beta) (Fc-gamma RIIIB)
DE   (FcRIIIB) (Fc-gamma RIII) (FcRIII) (CD16-B) (FcR-10).
GN   FCGR3B OR FCG3 OR FCGR3 OR IGFR3 OR CD16B.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (VARIANT NA-2).
RX   MEDLINE=89328325; PubMed=2526846;
RA   Ravetch J.V., Perussia B.;
RT   "Alternative membrane forms of Fc gamma RIII(CD16) on human natural
RT   killer cells and neutrophils. Cell type-specific expression of two
RT   genes that differ in single nucleotide substitutions.";
RL   J. Exp. Med. 170:481-497(1989).
RN   [2]
RP   SEQUENCE FROM N.A. (VARIANT NA-2).
RC   TISSUE=Placenta;
RX   MEDLINE=88232937; PubMed=2967436;
RA   Simmons D., Seed B.;
RT   "The Fc gamma receptor of natural killer cells is a phospholipid-
RT   linked membrane protein.";
RL   Nature 333:568-570(1988).
RN   [3]
RP   ERRATUM.
RA   Simmons D., Seed B.;
RL   Nature 340:662-662(1989).
RN   [4]
RP   SEQUENCE FROM N.A. (VARIANT NA-1).
RC   TISSUE=Leukocyte;
RX   MEDLINE=89128838; PubMed=2521732;
RA   Peltz G.A., Grundy H.O., Lebo R.V., Yssel H., Barsh G.S., Moore K.W.;
RT   "Human Fc-gamma-RIII: Cloning, expression, and identification of the
RT   chromosomal locus of two Fc receptors for IgG.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:1013-1017(1989).
RN   [5]
RP   SEQUENCE OF 1-72 FROM N.A. (VARIANT NA-2).
RC   TISSUE=Placenta;
RX   MEDLINE=95138131; PubMed=7836402;
RA   Gessner J.E., Grussenmeyer T., Kolanus W., Schmidt R.E.;
RT   "The human low affinity immunoglobulin G Fc receptor III-A and III-B
RT   genes. Molecular characterization of the promoter regions.";
RL   J. Biol. Chem. 270:1350-1361(1995).
RN   [6]
RP   X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS) IN COMPLEX WITH IGG1 FC.
RX   MEDLINE=20372189; PubMed=10917521;
RA   Sondermann P., Huber R., Oosthuizen V., Jacob U.;
RT   "The 3.2-A crystal structure of the human IgG1 Fc fragment-Fc
RT   gammaRIII complex.";
RL   Nature 406:267-273(2000).
RN   [7]
RP   X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 19-192.
RX   MEDLINE=20471519; PubMed=11021536;
RA   Zhang Y., Boesen C.C., Radaev S., Brooks A.G., Fridman W.H.,
RA   Sautes-Fridman C., Sun P.D.;
RT   "Crystal structure of the extracellular domain of a human Fc gamma
RT   RIII.";
RL   Immunity 13:387-395(2000).
RN   [8]
RP   VARIANT SH ASP-78.
RX   MEDLINE=97180159; PubMed=9028335;
RA   Bux J., Stein E.L., Bierling P., Fromont P., Clay M., Stroncek D.,
RA   Santoso S.;
RT   "Characterization of a new alloantigen (SH) on the human neutrophil Fc
RT   gamma receptor IIIb.";
RL   Blood 89:1027-1034(1997).
CC   -!- FUNCTION: RECEPTOR FOR THE FC REGION OF IMMUNOGLOBULINS GAMMA. LOW
CC       AFFINITY RECEPTOR. BINDS COMPLEXED OR AGGREGATED IGG AND ALSO
CC       MONOMERIC IGG. CONTRARY TO III-A, IS NOT CAPABLE TO MEDIATE
CC       ANTIBODY-DEPENDENT CYTOTOXICITY AND PHAGOCYTOSIS. MAY SERVE AS A
CC       TRAP FOR IMMUNE COMPLEXES IN THE PERIPHERAL CIRCULATION WHICH DOES
CC       NOT ACTIVATE NEUTROPHILS.
CC   -!- SUBUNIT: Monomer.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC       EXISTS ALSO AS A SOLUBLE RECEPTOR, PRODUCED BY A PROTEOLYTIC
CC       CLEAVAGE.
CC   -!- TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY BY POLYMORPHONUCLEAR
CC       LEUKOCYTES (NEUTROPHILS). ALSO EXPRESSED BY STIMULATED
CC       EOSINOPHILS.
CC   -!- PTM: GLYCOSYLATED. GLYCOSYLATION PLAYS AN INHIBITORY ROLE IN THE
CC       INTERACTION WITH IGG3.
CC   -!- PTM: The soluble form is produced by a proteolytic cleavage.
CC   -!- POLYMORPHISM: There are three allelic forms of FCGR3B: NA-1, NA-2
CC       (shown here) and SH. NA-1 and NA-2 are detectable with antibodies
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CC       against the biallelic neutrophil-specific antigen system NA.
CC   -!- DISEASE: The more active NA-1 allele has been associated with
CC       severe renal disease in certain systemic vasculitides.
CC   -!- MISCELLANEOUS: ENCODED BY ONE OF TWO NEARLY INDENTICAL GENES:
CC       FCGR3A AND FCGR3B (SHOWN HERE) WHICH ARE EXPRESSED IN A TISSUE-
CC       SPECIFIC MANNER. THE PHE-203 IN FCGR3A DETERMINES THE
CC       TRANSMEMBRANE DOMAINS WHEREAS THE SER-203 IN FCGR3B DETERMINES THE
CC       GPI-ANCHORING.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD16B entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd16b.htm".
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X16863; CAA34753.1; -.
DR   EMBL; X07934; CAA30758.1; -.
DR   EMBL; J04162; AAA35881.1; -.
DR   EMBL; Z46223; CAA86296.1; -.
DR   PIR; JU0284; JU0284.
DR   PDB; 1E4J; 04-AUG-00.
DR   PDB; 1E4K; 06-JUN-01.
DR   PDB; 1FNL; 22-NOV-00.
DR   PDB; 1IIS; 16-MAY-01.
DR   PDB; 1IIX; 16-MAY-01.
DR   Genew; HGNC:3620; FCGR3B.
DR   GO; GO:0006955; P:immune response; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   IgG-binding protein; Receptor; GPI-anchor; Glycoprotein; Signal;
KW   Immunoglobulin domain; Repeat; Multigene family; Polymorphism;
KW   3D-structure; Lipoprotein.
FT   SIGNAL       1    16       POTENTIAL.
FT   CHAIN       17   200       LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
FT                              REGION RECEPTOR III-B.
FT   PROPEP     201   233       REMOVED IN MATURE FORM (POTENTIAL).
FT   LIPID      200   200       GPI-anchor amidated serine (Potential).
FT   DOMAIN      40    96       IG-LIKE C2-TYPE 1.
FT   DOMAIN     121   179       IG-LIKE C2-TYPE 2.
FT   DISULFID    47    89
FT   DISULFID   128   172
FT   CARBOHYD    56    56       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    63    63       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    82    82       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    92    92       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   180   180       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   187   187       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     36    36       S -> R (in allele NA-1).
FT                              /FTId=VAR_003956.
FT   VARIANT     65    65       S -> N (in allele NA-1; dbSNP:448740).
FT                              /FTId=VAR_003963.
FT   VARIANT     78    78       A -> D (in allele SH).
FT                              /FTId=VAR_008802.
FT   VARIANT     82    82       N -> D (in allele NA-1).
FT                              /FTId=VAR_003957.
FT   VARIANT    106   106       I -> V (in allele NA-1).
FT                              /FTId=VAR_003964.
SQ   SEQUENCE   233 AA;  26216 MW;  7AB5159432761726 CRC64;

  Query Match             29.2%;  Score 406;  DB 1;  Length 233;
  Best Local Similarity   40.4%;  Pred. No. 1.8e-26;
  Matches   93;  Conservative   33;  Mismatches   94;  Indels   10;  Gaps    3;

Qy         10 LLCVALLFFAPDGVLAVPQKPK--VSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHN 67
              ||  |||     | :     ||  | | | |  : : ::||| | |    | :||:||||

Db          5 LLPTALLLLVSAG-MRTEDLPKAVVFLEPQWYSVLEKDSVTLKCQGAYSPEDNSTQWFHN 63

Qy         68 GSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQP 127
                ||      ||  |  |   |||||:||       |:|| |||   ||||||   |  | |

Db         64 ESLISSQASSYFIDAATVNDSGEYRCQTNLSTLSDPVQLEVHIGWLLLQAPRWVFKEEDP 123

Qy        128 LFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYES 187
              : |||| |:|  ::|| | ::|:  ||:: | :  |  ||::|||:|:| | |   :  |

Db        124 IHLRCHSWKNTALHKVTYLQNGKDRKYFHHNSDFHIPKATLKDSGSYFCRGLVGSKNVSS 183

Qy        188 EPLNITVIKAPREKYWLQFFIP-------LLVVILFAVDTGLFISTQQQV 230
              | :|||: :         |  |       |::|:|||||||: | :  :

Db        184 ETVNITITQGLAVSTISSFSPPGYQVSFCLVMVLLFAVDTGLYFSVKTNI 233


RESULT 8
FCG2_BOVIN
ID   FCG2_BOVIN     STANDARD;      PRT;   296 AA.
AC   Q28110;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Low affinity immunoglobulin gamma Fc region receptor II precursor (Fc-
DE   gamma RII) (FcRII) (IgG Fc receptor II).
GN   FCGR2.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=94245284; PubMed=8188320;
RA   Zhang G., Young J.R., Tregaskes C.R., Howard C.J.;
RT   "Cattle Fc gamma RII: molecular cloning and ligand specificity.";
RL   Immunogenetics 39:423-427(1994).
CC   -!- FUNCTION: Binds to the Fc region of immunoglobulins gamma. Low
CC       affinity receptor.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Higher expression is found in macrophages than
CC       in neutrophils (Probable).
CC   -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred
CC       to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC       This motif is involved in downmodulation of cellular responses.
CC       The phosphorylated ITIM motif binds to the SH2 domain of
CC       PTPN6/SHP-1.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X75671; CAA53367.1; -.
DR   PIR; I46021; I46021.
DR   HSSP; P12319; 1ALS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Immunoglobulin domain; Repeat.
FT   SIGNAL       1    42       POTENTIAL.
FT   CHAIN       43   296       LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
FT                              REGION RECEPTOR II.
FT   DOMAIN      43   225       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   226   246       POTENTIAL.
FT   DOMAIN     247   296       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      47   129       IG-LIKE C2-TYPE 1.
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FT   DOMAIN      130    212       IG-LIKE C2-TYPE 2.
FT   SITE        273    278       ITIM MOTIF.
FT   DISULFID     70    112       BY SIMILARITY.
FT   DISULFID    151    195       BY SIMILARITY.
FT   CARBOHYD     79     79       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     86     86       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    105    105       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    179    179       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    186    186       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    210    210       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   296 AA;  33020 MW;  A61A40A611F71ED5 CRC64;

  Query Match           29.1%;  Score 405;  DB 1;  Length 296;
  Best Local Similarity  42.2%;  Pred. No. 2.9e-26;
  Matches   79;  Conservative   33;  Mismatches   71;  Indels    4;  Gaps    2;

Qy         10 LLCVALLFFAPDGVLAVPQKPK--VSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHN 67
              ||  |||| ||  |   |  ||  |:: | |  : : ::||||| | :|   : | ||||
Db         29 LLWTALLFLAP--VSGKPDLPKAVVTIQPAWINVLREDHVTLTCQGTSFSAGNLTTWFHN 86

Qy         68 GSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQP 127
              ||              |  ||| |:|| :| : |:||:|:| ||||||| : |  ||:|
Db         87 GSSIHTQKQPSYSFRAGSNDSGSYRCQREQTSLSDPVHLDVISDWLLLQTPSLVFQEGEP 146

Qy        128 LFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYES 187
              : |||| |||  : |: :|:| ::  : |:  | ||  | :  || |:||  : :: : |
Db        147 IMLRCHSWRNQPLNKITFYQDRKSKIFSYQRTNFSIPRANLSHSGQYHCTAFIGKMLHSS 206

Qy        188 EPLNITV 194
              :|:||||
Db        207 QPVNITV 213


RESULT 9
FCG3_MOUSE
ID   FCG3_MOUSE     STANDARD;      PRT;   261 AA.
AC   P08508;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-AUG-1988 (Rel. 08, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Low affinity immunoglobulin gamma Fc region receptor III precursor
DE   (IgG Fc receptor III) (Fc-gamma RIII) (FcRIII).
GN   FCGR3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87042761; PubMed=2946078;
RA   Ravetch J.V., Luster A.D., Weinshank R., Kochan J., Pavlovec A.,
RA   Portnoy D.A., Hulmes J., Pan Y.-C.E., Unkeless J.C.;
RT   "Structural heterogeneity and functional domains of murine
RT   immunoglobulin G Fc receptors.";
RL   Science 234:718-725(1986).
RN   [2]
RP   SEQUENCE OF 1-29 FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Liver;
RA   Soares H.J., Onken M.D., Kulczycki A. Jr.;
RL   Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Receptor for the Fc region of complexed immunoglobulins
CC       gamma. Low affinity receptor.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M14215; AAA37604.1; -.
DR   EMBL; X60929; CAA43266.1; -.
DR   PIR; S29360; S29360.
DR   HSSP; P12319; 1ALS.
DR   MGD; MGI:95500; Fcgr3.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Immunoglobulin domain; Repeat.
FT   SIGNAL        1     30       POTENTIAL.
FT   CHAIN        31    261       LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
FT                                REGION RECEPTOR III.
FT   DOMAIN       31    215       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    216    235       POTENTIAL.
FT   DOMAIN      236    261       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       33    110       IG-LIKE C2-TYPE 1.
FT   DOMAIN      116    198       IG-LIKE C2-TYPE 2.
FT   DISULFID     56     98       BY SIMILARITY.
FT   DISULFID    137    181       BY SIMILARITY.
FT   CARBOHYD     64     64       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     91     91       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    165    165       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    172    172       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   261 AA;  30036 MW;  757FB83668E41069 CRC64;

  Query Match           28.9%;  Score 401.5;  DB 1;  Length 261;
  Best Local Similarity  35.6%;  Pred. No. 4.8e-26;
  Matches   90;  Conservative   44;  Mismatches  104;  Indels   15;  Gaps    5;

Qy         11 LCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNG-S 69
              | : |||   |   |   |  | |:||| :: | : ||| | | :    |||:||||| |
Db         16 LTILLLFAFADRQSAALPKAVVKLDPPWIQVLKEDMVTLMCEGTHNPGNSSTQWFHNGRS 75

Qy         70 LSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLF 129
              :  :  :|      |  |||||:|| :|   |:|| | | |||||||     | :||: :
Db         76 IRSQVQASYTF-KATVNDSGEYRCQMEQTRLSDPVDLGVISDWLLLQTPQRVFLEGETIT 134

Qy        130 LRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEP 189
              |||| |||  : :: :: : ::::| :   | ||  |    || ||| | :    ::|:|
Db        135 LRCHSWRNKLLNRISFFHNEKSVRYHHYKSNFSIPKANHSHSGDYYCKGSLGSTQHQSKP 194

Qy        190 LNITV----IKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFR- 244
              : |||     :     |    |:: :||||||:   ::       ::  |: :|
Db        195 VTITVQDPATTSSISLVWYHTAFSLVMCLLFAVDTGLYFYVRR------NLQTPREYWRK 248

Qy        245 --LLNPHPKPNPK 255
                :  |  |  |
Db        249 SLSIRKHQAPQDK 261


RESULT 10
FCG3_RAT
ID   FCG3_RAT       STANDARD;      PRT;   267 AA.
AC   P27645; Q04798; Q63204;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Low affinity immunoglobulin gamma Fc region receptor III precursor
DE   (IgG Fc receptor III) (Fc-gamma RIII) (FcRIII).
GN   FCGR3.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS B; C AND D).
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=91250730; PubMed=1710249;
RA   Farber D.L., Sears D.W.;
RT   "Rat CD16 is defined by a family of class III Fc gamma receptors
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RT   requiring co-expression of heteroprotein subunits.";
RL   J. Immunol. 146:4352-4361(1991).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM A).
RC   TISSUE=Natural killer cells;
RX   MEDLINE=90239026; PubMed=1692135;
RA   Zeger D.L., Hogarth P.M., Sears D.W.;
RT   "Characterization and expression of an Fc gamma receptor cDNA cloned
RT   from rat natural killer cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:3425-3429(1990).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM H).
RC   STRAIN=Sprague-Dawley; TISSUE=Brain;
RX   MEDLINE=93246650; PubMed=8482840;
RA   Farber D.L., Giorda R., Nettleton M.Y., Trucco M., Kochan J.P.,
RA   Sears D.W.;
RT   "Rat class III Fc gamma receptor isoforms differ in IgG subclass-
RT   binding specificity and fail to associate productively with rat CD3
RT   zeta.";
RL   J. Immunol. 150:4364-4375(1993).
CC   -!- FUNCTION: Receptor for the Fc region of complexed immunoglobulins
CC       gamma. Low affinity receptor.
CC   -!- SUBUNIT: MAY FORM MULTISUBUNIT COMPLEX WITH OTHER HETEROPROTEINS.
CC       THIS ASSOCIATION IS REQUIRED FOR EFFICIENT CELL-SURFACE
CC       EXPRESSION. DOES NOT ASSOCIATE WITH CD3 ZETA.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=8;
CC         Comment=Additional isoforms seem to exist;
CC       Name=C;
CC         IsoId=P27645-1; Sequence=Displayed;
CC       Name=A;
CC         IsoId=P27645-3; Sequence=Not described;
CC       Name=B;
CC         IsoId=P27645-4; Sequence=Not described;
CC       Name=D;
CC         IsoId=P27645-5; Sequence=Not described;
CC       Name=E;
CC         IsoId=P27645-6; Sequence=Not described;
CC       Name=F;
CC         IsoId=P27645-7; Sequence=Not described;
CC       Name=G;
CC         IsoId=P27645-8; Sequence=Not described;
CC       Name=H;
CC         IsoId=P27645-2; Sequence=VSP_002647;
CC   -!- TISSUE SPECIFICITY: EXPRESSED ON NATURAL KILLERS CELLS AND
CC       MACROPHAGES.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M64368; AAA42049.1; -.
DR   EMBL; M64369; AAA42048.1; -.
DR   EMBL; M64370; AAA42050.1; -.
DR   EMBL; M32062; AAA41148.1; -.
DR   EMBL; L08446; AAA41151.1; -.
DR   PIR; A35902; A35902.
DR   PIR; I56110; I56110.
DR   HSSP; P12319; 1ALS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Immunoglobulin domain; Repeat; Alternative splicing.
FT   SIGNAL        1     36       POTENTIAL.
FT   CHAIN         37    267      LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
FT                                REGION RECEPTOR III.
FT   DOMAIN        37    221      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      222   241      POTENTIAL.
FT   DOMAIN        242   267      CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        39    121      IG-LIKE C2-TYPE 1.
FT   DOMAIN        122   204      IG-LIKE C2-TYPE 2.
FT   DISULFID      62    104      BY SIMILARITY.
FT   DISULFID      143   187      BY SIMILARITY.
FT   VARSPLIC      145   176      SWKNKQLTKVLLFQNGKPVRYYYQSSNFSIPK -> GWKSI
FT                                QLARISFLQNGEFVSFHPYNVSYSISN (in isoform
FT                                H).
FT                                /FTId=VSP_002647.
FT   VARIANT       36    39       ANLP -> GDLL (IN ISOFORM A AND ISOFORM
FT                                H).
FT   VARIANT       55    55       E -> D (IN ISOFORM A AND ISOFORM H).
FT   VARIANT       56    56       D -> G (IN ISOFORM D).
FT   VARIANT       115   115      V -> I (IN ISOFORM A AND ISOFORM B).
FT   VARIANT       134   134      E -> L (IN ISOFORM H).
FT   VARIANT       138   138      T -> R (IN ISOFORM H).
FT   VARIANT       184   184      N -> D (IN ISOFORM H).
FT   VARIANT       195   195      M -> E (IN ISOFORM H).
FT   VARIANT       254   254      K -> R (IN ISOFORM H).
SQ   SEQUENCE   267 AA;  30281 MW;  DD4D6A7A3F70ED92 CRC64;

  Query Match             28.8%;  Score 400;  DB 1;  Length 267;
  Best Local Similarity   37.5%;  Pred. No. 6.6e-26;
  Matches   84;  Conservative   41;  Mismatches   95;  Indels    4;  Gaps    1;

Qy          11 LCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSL 70
               | : |||    |    |    |  |  :||| :: | : ||||| | :    |||:|||| |
Db          22 LTMLLLFAFADRQTANLPKAVVKRDPPWIQVLKEDTVTLTCEGTHNPGNSSTQWFHNQSS 81

Qy          71 SEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFL 130
               :    :      |   |||||:|:    : |:||:||| |||||||    |  ||: : |
Db          82 TWGQVQASYTFKATVNDSGEYRCRMAHTSLSDPVHLEVISDWLLLQTPQLVFEEGETITL 141

Qy         131 RCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPL 190
               ||| |:|  : ||: :::|: ::|:|:: | ||  |    || |||    : :  : |:|:
Db         142 RCHSWKNKQLTKVLLFQNGKPVRYYYQSSNFSIPKANHSHSGNYYCKAYLGRTMHVSKPV 201

Qy         191 NITV----IKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQV 230
                 |||       :     |       |:: :||||||||:   :: :
Db         202 TITVQGSATASTSSLVWFHAAFCLVMCLLFAVDTGLYFCVRRNL 245


RESULT 11
FCG2_CAVPO
ID   FCG2_CAVPO     STANDARD;      PRT;   341 AA.
AC   Q60513; Q60498; Q60511; Q60512;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Low affinity immunoglobulin gamma Fc region receptor II precursor (Fc-
DE   gamma RII) (FcRII) (IgG Fc receptor II) (Fc-gamma-1/gamma-2 receptor).
GN   FCGR2.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 2R-B1).
RX   MEDLINE=90241239; PubMed=1692213;
RA   Tominaga M., Sakata A., Ohmura T., Yamashita T., Koyama J., Onoue K.;
RT   "The structure and expression of the guinea pig Fc receptor for IgG1
RT   and IgG2 (Fc gamma 1/gamma 2R).";
RL   Biochem. Biophys. Res. Commun. 168:683-689(1990).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 2R-B1; 2R-B2 AND 2R-B3).
RC   STRAIN=JY-1;
RX   MEDLINE=93346746; PubMed=8345193;
RA   Yamashita T., Shinohara K., Yamashita Y.;
RT   "Expression cloning of complementary DNA encoding three distinct
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RT   isoforms of guinea pig Fc receptor for IgG1 and IgG2.";
RL   J. Immunol. 151:2014-2023(1993).
CC   -!- FUNCTION: Binds to the Fc region of immunoglobulins gamma. Low
CC       affinity receptor.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=2R-B3;
CC         IsoId=Q60513-1; Sequence=Displayed;
CC       Name=2R-B1;
CC         IsoId=Q60513-2; Sequence=VSP_002639;
CC       Name=2R-B2;
CC         IsoId=Q60513-3; Sequence=VSP_002638;
CC   -!- TISSUE SPECIFICITY: Macrophages and polymorphonuclear leukocytes
CC       express preferentially isoform 2R-B1. B lymphocytes express
CC       isoform 2R-B1, isoform 2R-B2 and isoform 2R-B3.
CC   -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred
CC       to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC       This motif is involved in downmodulation of cellular responses.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D13693; BAA02852.1; -.
DR   EMBL; D13692; BAA02851.1; -.
DR   EMBL; D13691; BAA02850.1; -.
DR   EMBL; M35272; AAA37036.1; ALT_INIT.
DR   HSSP; P12319; 1ALS.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Immunoglobulin domain; Repeat; Alternative splicing.
FT   SIGNAL        1     42       POTENTIAL.
FT   CHAIN        43    341       LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
FT                                 REGION RECEPTOR II.
FT   DOMAIN       43    224       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    225    245       POTENTIAL.
FT   DOMAIN      246    341       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       48    125       IG-LIKE C2-TYPE 1.
FT   DOMAIN      131    213       IG-LIKE C2-TYPE 2.
FT   SITE        318    323       ITIM MOTIF.
FT   DISULFID     71    113       BY SIMILARITY.
FT   DISULFID    152    196       BY SIMILARITY.
FT   CARBOHYD     79     79       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    106    106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    180    180       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    187    187       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    195    195       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    273    301       GEYSVVFGGSMMSCPGLPDGLEPARTDLS -> A (in
FT                                 isoform 2R-B2).
FT                                 /FTId=VSP_002638.
FT   VARSPLIC    257    301       GNPEHREMGETLPEDPGEYSVVFGGSMMSCPGLPDGLEPAR
FT                                 TDLS -> A (in isoform 2R-B1).
FT                                 /FTId=VSP_002639.
FT   CONFLICT    114    114       Q -> QVLPSYRFTAKGNDSGEYRCQ (IN REF. 1).
SQ   SEQUENCE   341 AA;  37091 MW;  5137E3271D443B84 CRC64;

  Query Match             28.4%;  Score 395;  DB 1;  Length 341;
  Best Local Similarity   38.2%;  Pred. No. 2.3e-25;
  Matches   96;  Conservative   33;  Mismatches  106;  Indels   16;  Gaps    5;

Qy          7 SPTLLCVALLFFAP-DGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWF 65
              |  || : :|| ||  |  | | |  | | ||| :: :|: ||||| |      ||:|
Db         26 SHMLLWITVLFLAPVAGTSADPPKAVVRLEPPWIQVLRGDRVTLTCEGAPSPGNHSTQWL 85

Qy         66 HNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEG 125
                ||| |            ||  |||||:||    : |:|| |:| ||||:|| |  :  ||
Db         86 HNGRLIPTQVLPSYRFTAKGNDSGEYRCQAGGTSLSDPVRLDVISDWLVLQTSQLIFQEG 145

Qy        126 QPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDY 185
               : |||| | || : || :| :| | ||:  : | ||  |    || | ||| : :  :
Db        146 DVIVLRCHSWNNWPLAKVTFYHNGVAKKYFSISKNFSIPQANHSHSGAYNCTGLIGRTSH 205

Qy        186 ESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRL 245
               | |: ||| : |:          :|||: |   |  |:|   |  :: |   :|
Db        206 TSPPVTITV-QGPKSS------DSSMVVIIVAAVIG--IATAAIVVAVVAIICLKK---- 252

Qy        246 LNPHPKPNPKN 256
                 |  ||::
Db        253 --KQPPGNPEH 261


RESULT 12
FCG1_HUMAN
ID   FCG1_HUMAN     STANDARD;      PRT;   374 AA.
AC   P12314; P12315;
DT   01-OCT-1989 (Rel. 12, Created)
DT   01-OCT-1989 (Rel. 12, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   High affinity immunoglobulin gamma Fc receptor I precursor (Fc-gamma
DE   RI) (FcRI) (IgG Fc receptor I) (CD64 antigen).
GN   FCGR1A OR FCGR1 OR FCG1 OR IGFR1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89098339; PubMed=2974947;
RA   Allen J.M., Seed B.;
RT   "Nucleotide sequence of three cDNAs for the human high affinity Fc
RT   receptor (FcRI).";
RL   Nucleic Acids Res. 16:11824-11824(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89100284; PubMed=2911749;
RA   Allen J.M., Seed B.;
RT   "Isolation and expression of functional high-affinity Fc receptor
RT   complementary DNAs.";
RL   Science 243:378-381(1989).
CC   -!- FUNCTION: Binds to the Fc region of immunoglobulins gamma. High
CC       affinity receptor.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=A;
CC         IsoId=P12314-1; Sequence=Displayed;
CC       Name=B;
CC         IsoId=P12314-2; Sequence=VSP_002637;
CC   -!- TISSUE SPECIFICITY: Monocyte/macrophage specific.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD64 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd64.htm".
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X14356; CAA32537.1; -.
DR   EMBL; X14355; CAA32536.1; -.
DR   PIR; A41357; A41357.
DR   HSSP; P12319; 1ALS.
DR   Genew; HGNC:3613; FCGR1A.
DR   MIM; 146760; -.
DR   GO; GO:0005057; F:receptor signaling protein activity; TAS.
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DR   GO; GO:0006955; P:immune response; TAS.
DR   GO; GO:0006911; P:phagocytosis, engulfment; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003599; Ig.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Immunoglobulin domain; Repeat; Alternative splicing; Polymorphism.
FT   SIGNAL        1     21
FT   CHAIN        22    374       HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC
FT                                 RECEPTOR I.
FT   DOMAIN       22    292       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    293    313       POTENTIAL.
FT   DOMAIN      314    374       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       22    101       IG-LIKE C2-TYPE 1.
FT   DOMAIN       95    184       IG-LIKE C2-TYPE 2.
FT   DOMAIN      190    277       IG-LIKE C2-TYPE 3.
FT   DISULFID     43     85       BY SIMILARITY.
FT   DISULFID    124    168       BY SIMILARITY.
FT   DISULFID    212    260       BY SIMILARITY.
FT   CARBOHYD     59     59       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     78     78       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    152    152       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    159    159       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    163    163       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    195    195       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    240    240       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC    333    374       HEKKVTSSLQEDRHLEEELKCQEQKEEQLQEGVHRKEPQGA
FT                                 T -> GQALEAPTQGCA (in isoform B).
FT                                 /FTId=VSP_002637.
FT   VARIANT      26     26       L -> T.
FT                                 /FTId=VAR_003953.
FT   VARIANT      59     59       N -> V.
FT                                 /FTId=VAR_003954.
FT   CONFLICT     25     25       S -> T (IN REF. 1; CAA32536).
SQ   SEQUENCE   374 AA;  42605 MW;  2C2AA8103ECF16E6 CRC64;

  Query Match             27.3%;  Score 379;  DB 1;  Length 374;
  Best Local Similarity   40.2%;  Pred. No. 5.3e-24;
  Matches   74;  Conservative   38;  Mismatches   70;  Indels    2;  Gaps    2;

Qy          11 LCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSL 70
               |    ||:   || :    |  :|| |||  :|: | ||| |   :     |||:|| ||:
Db           4 LTTLLLWVPVDGQVDT-TKAVISLQPPWVSVFQEETVTLHCEVLHLPGSSSTQWFLNGTA 62

Qy          71 SEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFL 130
               :: :  |  | :|   |||||:||      |:|: ||:   ||||| |: |  ||:|| |
Db          63 TQTSTPSYRITSASVNDSGEYRCQRGLSGRSDPIQLEIHRGWLLLQVSSRVFTEGEPLAL 122

Qy         131 RCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPL 190
               ||| |::  || |:||::|:| |::: | |::|    :  :|||:|:| : :  | |  :
Db         123 RCHAWKDKLVYNVLYYRNGKAFKFFHWNSNLTILKTNISHNGTYHCSG-MGKHRYTSAGI 181

Qy         191 NITV 194
               ::||
Db         182 SVTV 185


RESULT 13
FCG1_MOUSE
ID   FCG1_MOUSE     STANDARD;      PRT;   404 AA.
AC   P26151;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   High affinity immunoglobulin gamma Fc receptor I precursor (Fc-gamma
DE   RI) (FcRI) (IgG Fc receptor I).
GN   FCGR1 OR FCG1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90111035; PubMed=2136886;
RA   Sears D.W., Osman N., Tate B., McKenzie I.F.C., Hogarth P.M.;
RT   "Molecular cloning and expression of the mouse high affinity Fc
RT   receptor for IgG.";
RL   J. Immunol. 144:371-378(1990).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92166399; PubMed=1531670;
RA   Osman N., Kozak C.A., McKenzie I.F., Hogarth P.M.;
RT   "Structure and mapping of the gene encoding mouse high affinity Fc
RT   gamma RI and chromosomal location of the human Fc gamma RI gene.";
RL   J. Immunol. 148:1570-1575(1992).
CC   -!- FUNCTION: Binds to the Fc region of immunoglobulins gamma. High
CC       affinity receptor.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: Macrophage specicic.
CC   -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC   -!- CAUTION: It is uncertain whether Met-1 or Met-10 is the initiator.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M31314; AAA40056.1; -.
DR   PIR; A46480; A46480.
DR   HSSP; P12319; 1ALS.
DR   MGD; MGI:95498; Fcgr1.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Immunoglobulin domain; Repeat.
FT   SIGNAL        1     24
FT   CHAIN        25    404       HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC
FT                                 RECEPTOR I.
FT   DOMAIN       25    297       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    298    320       POTENTIAL.
FT   DOMAIN      321    404       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       32    111       IG-LIKE C2-TYPE 1.
FT   DOMAIN      117    194       IG-LIKE C2-TYPE 2.
FT   DOMAIN      201    286       IG-LIKE C2-TYPE 3.
FT   DISULFID     53     95       BY SIMILARITY.
FT   DISULFID    134    177       BY SIMILARITY.
FT   DISULFID    221    269       BY SIMILARITY.
FT   CARBOHYD     28     28       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     48     48       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     69     69       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    168    168       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    249    249       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   404 AA;  44887 MW;  1C4F0033842767E7 CRC64;

  Query Match             27.3%;  Score 379;  DB 1;  Length 404;
  Best Local Similarity   41.6%;  Pred. No. 5.8e-24;
  Matches   77;  Conservative   37;  Mismatches   69;  Indels    2;  Gaps    2;

Qy          10 LLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGS 69
               ||   ||:    | :    |  ::| |||  ||: ||||| | | :    |||:|| ||:
Db          12 LLTTLLLWVPVGGEVVNATKAVITLQPPWVSIFQKENVTLWCEGPHLPGDSSTQWFINGT 71

Qy          70 LSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLF 129
                 : :  | :|  | |:|||||:||      |:|| |:: :||||||||  |: ||:||
Db          72 AVQISTPSYSIPEASFQDSGEYRCQIGSSMPSDPVQLQIHNDWLLLQASRRVLTEGEPLA 131

Qy         130 LRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEP 189
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                ||||||:|  || |::|::|:: ::   :  ::|    :  || |:|:|   :  | |
Db        132 LRCHGWKNKLVYNVVFYRNGKSFQF-SSDSEVAILKTNLSHSGIYHCSG-TGRHRYTSAG 189

Qy        190 LNITV 194
              ::|||
Db        190 VSITV 194


RESULT 14
FCGB_HUMAN
ID   FCGB_HUMAN     STANDARD;      PRT;   310 AA.
AC   P31994; O95649; Q8NIA1;
DT   01-JUL-1993 (Rel. 26, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Low affinity immunoglobulin gamma Fc region receptor II-b precursor
DE   (Fc-gamma RII-b) (FcRII-b) (IgG Fc receptor II-b) (Fc-gamma-RIIb)
DE   (CD32 antigen) (CDw32).
GN   FCGR2B OR FCG2 OR IGFR2 OR CD32.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS IIB1 AND IIB2).
RC   TISSUE=Lymphocytes;
RA   Ng S., Sinclair N.R.S., Anderson C., Bell D.A., Cairns E.;
RT   "Fc-gamma-RIIb nucleotide sequences in SLE and non-SLE humans in vivo
RT   derived lymphocytes.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM IIB2).
RC   TISSUE=Placenta;
RX   MEDLINE=90059965; PubMed=2531080;
RA   Stuart S.G., Simister N.E., Clarkson S.B., Kacinski B.M., Shapiro M.,
RA   Mellman I.;
RT   "Human IgG Fc receptor (hFcRII; CD32) exists as multiple isoforms in
RT   macrophages, lymphocytes and IgG-transporting placental epithelium.";
RL   EMBO J. 8:3657-3666(1989).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS IIB1; IIB2 AND IIB3).
RX   MEDLINE=90010791; PubMed=2529342;
RA   Brooks D.G., Qiu W.Q., Luster A.D., Ravetch J.V.;
RT   "Structure and expression of human IgG FcRII(CD32). Functional
RT   heterogeneity is encoded by the alternatively spliced products of
RT   multiple genes.";
RL   J. Exp. Med. 170:1369-1385(1989).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM IIB2).
RC   TISSUE=Placenta;
RX   MEDLINE=90316181; PubMed=2142460;
RA   Engelhardt W., Geerds C., Frey J.;
RT   "Distribution, inducibility and biological function of the cloned and
RT   expressed human beta Fc receptor II.";
RL   Eur. J. Immunol. 20:1367-1377(1990).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM IIB1).
RC   TISSUE=Skin;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   SEQUENCE OF 132-253 FROM N.A., AND VARIANT THR-232.
RX   MEDLINE=22109090; PubMed=12115230;
RA   Kyogoku C., Dijstelbloem H.M., Tsuchiya N., Hatta Y., Kato H.,
RA   Yamaguchi A., Fukazawa T., Jansen M.D., Hashimoto H.,
RA   van de Winkel J.G.J., Kallenberg C.G.M., Tokunaga K.;
RT   "Fc gamma receptor gene polymorphisms in Japanese patients with
RT   systemic lupus erythematosus: contribution of FCGR2B to genetic
RT   susceptibility.";
RL   Arthritis Rheum. 46:1242-1254(2002).
RN   [7]
RP   VARIANT ASP-258.
RX   MEDLINE=93222096; PubMed=8466861;
RA   Warmerdam P.A., van den Herik-Oudijk I.E., Parren P.W.,
RA   Westerdaal N.A., van de Winkel J.G., Capel P.J.;
RT   "Interaction of a human Fc gamma RIIb1 (CD32) isoform with murine and
RT   human IgG subclasses.";
RL   Int. Immunol. 5:239-247(1993).
CC   -!- FUNCTION: Receptor for the Fc region of complexed or aggregated
CC       immunoglobulins gamma. Low affinity receptor. Involved in a
CC       variety of effector and regulatory functions such as phagocytosis
CC       of immune complexes and modulation of antibody production by B-
CC       cells. Binding to this receptor results in downmodulation of
CC       previous state of cell activation triggered via antigen receptors
CC       on B cells (BCR), T cells (TCR) or via another Fc receptor.
CC       Isoform IIB1 fails to mediate endocytosis or phagocytosis. Isoform
CC       IIB2 does not trigger phagocytosis.
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=IIB1;
CC         IsoId=P31994-1; Sequence=Displayed;
CC       Name=IIB2;
CC         IsoId=P31994-2; Sequence=VSP_002643;
CC       Name=IIB3;
CC         IsoId=P31994-3; Sequence=VSP_002642;
CC   -!- TISSUE SPECIFICITY: Is the most broadly distributed Fc-gamma-
CC       receptor. Expressed in monocyte, neutrophils, macrophages,
CC       basophils, eosinophils, Langerhans cells, B cells, platelets
CC       cells and placenta (endothelial cells). Not detected in natural
CC       killer cells.
CC   -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred
CC       to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
CC       This motif is involved in downmodulation of cellular responses.
CC       The phosphorylated ITIM motif binds to the SH2 domain of
CC       PTPN6/SHP-1.
CC   -!- DISEASE: Involved in a follicular lymphoma through a chromosomal
CC       translocation t(1;22)(q22;q11) which leads to the hyperexpression
CC       of the receptor. This may play a role in the tumor progression.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   -!- CAUTION: Has sometime been attributed to correspond to FCR-IIC.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD32 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd32.htm".
CC   -!- DATABASE: NAME=Atlas Genet. Cytogenet. Oncol. Haematol.;
CC       WWW="http://www.infobiogen.fr/services/chromcancer/Genes/FCGR2BID397.html".
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; U87560; AAD00627.1; -.
DR   EMBL; U87561; AAD00628.1; -.
DR   EMBL; U87562; AAD00629.1; -.
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DR   EMBL; U87563; AAD00630.1; -.
DR   EMBL; U87564; AAD00631.1; -.
DR   EMBL; U87565; AAD00632.1; -.
DR   EMBL; U87566; AAD00633.1; -.
DR   EMBL; U87567; AAD00634.1; -.
DR   EMBL; U87568; AAD00635.1; -.
DR   EMBL; U87569; AAD00636.1; -.
DR   EMBL; U87570; AAD00637.1; -.
DR   EMBL; U87571; AAD00638.1; -.
DR   EMBL; U87572; AAD00639.1; -.
DR   EMBL; U87573; AAD00640.1; -.
DR   EMBL; U87574; AAD00641.1; -.
DR   EMBL; U87575; AAD00642.1; -.
DR   EMBL; U87576; AAD00643.1; -.
DR   EMBL; U87577; AAD00644.1; -.
DR   EMBL; X17653; CAA35644.1; -.
DR   EMBL; X17653; CAA35645.1; ALT_INIT.
DR   EMBL; M31933; AAA35841.1; -.
DR   EMBL; M31934; AAA35842.1; -.
DR   EMBL; M31935; AAA35843.1; -.
DR   EMBL; X52473; CAA36713.1; -.
DR   EMBL; BC031992; AAH31992.1; -.
DR   EMBL; AB050934; BAB92093.1; -.
DR   PIR; JL0119; JL0119.
DR   PDB; 2FCB; 01-MAR-00.
DR   Genew; HGNC:3618; FCGR2B.
DR   MIM; 604590; -.
DR   GO; GO:0015029; F:internalization receptor activity; TAS.
DR   GO; GO:0006955; P:immune response; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Immunoglobulin domain; Repeat; Multigene family; Alternative splicing;
KW   Polymorphism; Chromosomal translocation; Proto-oncogene; 3D-structure.
FT   SIGNAL        1    42       POTENTIAL.
FT   CHAIN        43   310       LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
FT                               REGION RECEPTOR II-B.
FT   DOMAIN        43   217       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM     218   240       POTENTIAL.
FT   DOMAIN       241   310       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        48   127       IG-LIKE C2-TYPE 1.
FT   DOMAIN       131   213       IG-LIKE C2-TYPE 2.
FT   SITE         290   295       ITIM MOTIF.
FT   DISULFID      71   113       BY SIMILARITY.
FT   DISULFID     152   196       BY SIMILARITY.
FT   CARBOHYD     106   106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     180   180       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     187   187       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      39    45       Missing (in isoform IIB3).
FT                               /FTId=VSP_002642.
FT   VARSPLIC     255   273       Missing (in isoform IIB2).
FT                               /FTId=VSP_002643.
FT   VARIANT      232   232       I -> T.
FT                               /FTId=VAR_015515.
FT   VARIANT      258   258       Y -> D.
FT                               /FTId=VAR_008798.
FT   CONFLICT      46    46       MISSING (IN REF. 1; AAD00637/AAD00638/
FT                               AAD00639/AAD00644).
FT   CONFLICT     178   178       D -> I (IN REF. 2).
FT   CONFLICT     205   205       Y -> F (IN REF. 3).
FT   CONFLICT     230   230       T -> I (IN REF. 2).
FT   CONFLICT     242   242       V -> G (IN REF. 2).

  Query Match           26.7%;  Score 371.5;  DB 1;  Length 310;
  Best Local Similarity  37.3%;  Pred. No. 1.8e-23;
  Matches   81;  Conservative   39;  Mismatches   86;  Indels   11;  Gaps    4;

Qy         10 LLCVALLFFAP-DGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNG 68
              ||   |:|| ||  |  | | | | : | | |  : : ::||||| | :  |  | :|||||
Db         29 LLWTAVLFLAPVAGTPAAPPKAVLKLEPQWINVLQEDSVTLTCRGTHSPESDSIQWFHNG 88

Qy         69 SLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPL 128
              :|          |   ||||| ||  | : |:||:| | |:||:||       ||: :
Db         89 NLIPTHTQPSYRFKANNNDSGEYTCQTGQTSLSDPVHLTVLSEWLVLQTPHLEFQEGETI 148

Qy        129 FLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESE 188
              |||| |::  : || ::::|:: |:   : | ||  |     || |:||| :    | |:
Db        149 VLRCHSWKDKPLVKVTFFQNGKSKKFSRSDPNFSIPQANHSHSGDYHCTGNIGYTLYSSK 208

Qy        189 PLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFIS 225
              |: ||| :||           |: :::  || ||: ::
Db        209 PVTITV-QAPSSS-------PMGIIV--AVVTGIAVA 235


RESULT 15
FCGC_HUMAN
ID   FCGC_HUMAN     STANDARD;      PRT;   323 AA.
AC   P31995; O00523; O00524; O00525;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Low affinity immunoglobulin gamma Fc region receptor II-c precursor
DE   (Fc-gamma RII-c) (FcRII-c) (IgG Fc receptor II-c) (Fc-gamma-RIIc)
DE   (CD32 antigen) (CDw32).
GN   FCGR2C OR FCG2 OR IGFR2 OR CD32.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM IIC/C1).
RC   TISSUE=Placenta;
RX   MEDLINE=90059965; PubMed=2531080;
RA   Stuart S.G., Simister N.E., Clarkson S.B., Kacinski B.M., Shapiro M.,
RA   Mellman I.;
RT   "Human IgG Fc receptor (hFcRII; CD32) exists as multiple isoforms in
RT   macrophages, lymphocytes and IgG-transporting placental epithelium.";
RL   EMBO J. 8:3657-3666(1989).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS IIC/C1; IIC2; IIC3 AND IIC4).
RC   TISSUE=Natural killer cells;
RX   MEDLINE=98182301; PubMed=9516136;
RA   Metes D., Ernst L.K., Chambers W.H., Sulica A., Herberman R.B.,
RA   Morel P.A.;
RT   "Expression of functional CD32 molecules on human NK cells is
RT   determined by an allelic polymorphism of the FcgammaRIIC gene.";
RL   Blood 91:2369-2380(1998).
CC   -!- FUNCTION: RECEPTOR FOR THE FC REGION OF COMPLEXED IMMUNOGLOBULINS
CC       GAMMA. LOW AFFINITY RECEPTOR. INVOLVED IN A VARIETY OF EFFECTOR
CC       AND REGULATORY FUNCTIONS SUCH AS PHAGOCYTOSIS OF IMMUNE COMPLEXES
CC       AND MODULATION OF ANTIBODY PRODUCTION BY B-CELLS.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORMS IIC1,
CC       IIC2, AND IIC3). ISOFORM IIC4 MAY BE A SOLUBLE FORM.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=IIC; Synonyms=C1;
CC         IsoId=P31995-1; Sequence=Displayed;
CC       Name=IIC2;
CC         IsoId=P31995-2; Sequence=VSP_002646;
CC       Name=IIC3;
CC         IsoId=P31995-3; Sequence=VSP_002645;
CC       Name=IIC4;
CC         IsoId=P31995-4; Sequence=VSP_002644;
CC   -!- TISSUE SPECIFICITY: ISOFORM IIC1 IS DETECTED IN MONOCYTES,
CC       MACROPHAGES, POLYMORPHONUCLEAR CELLS AND NATURAL KILLER CELLS.
CC   -!- DOMAIN: CONTAINS AN INTRACYTOPLASMIC TWICE REPEATED MOTIF REFERRED
CC       AS IMMUNORECEPTOR TYROSINE-BASED ACTIVATOR MOTIF (ITAM). THESE
CC       MOTIFS ARE INVOLVED IN TRIGGERING CELL ACTIVATION UPON RECEPTORS
CC       AGGREGATION.
CC   -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC   -!- CAUTION: HAS SOMETIME BEEN ATTRIBUTED TO CORRESPOND TO FCR-IIB.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD32 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd32.htm".
CC   ---------------------------------------------------------------------
```

```
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; X17652; CAA35642.1; -.
DR   EMBL; X17652; CAA35643.1; ALT_INIT.
DR   EMBL; U90938; AAC12807.1; -.
DR   EMBL; U90939; AAC12808.1; -.
DR   EMBL; U90940; AAC12809.1; -.
DR   EMBL; U90941; AAC12810.1; -.
DR   PIR; S06946; S06946.
DR   HSSP; P12319; 1ALS.
DR   GO; GO:0016021; C:integral to membrane; NAS.
DR   GO; GO:0004888; F:transmembrane receptor activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   IgG-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW   Immunoglobulin domain; Repeat; Multigene family; Alternative splicing.
FT   SIGNAL        1     42       POTENTIAL.
FT   CHAIN         43    323      LOW AFFINITY IMMUNOGLOBULIN GAMMA FC
FT                                REGION RECEPTOR II-C.
FT   DOMAIN        43    223      EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM      224   246      POTENTIAL.
FT   DOMAIN        247   323      CYTOPLASMIC (POTENTIAL).
FT   DOMAIN        48    127      IG-LIKE C2-TYPE 1.
FT   DOMAIN        131   213      IG-LIKE C2-TYPE 2.
FT   DOMAIN        294   313      ITAM MOTIF.
FT   DISULFID      71    113      BY SIMILARITY.
FT   DISULFID      152   196      BY SIMILARITY.
FT   CARBOHYD      106   106      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      180   180      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD      187   187      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARSPLIC      216   323      APSSSPMGIIVAVVTGIAVAAIVAAVVALIYCRKKRISANS
FT                                TDPVKAAQFEPPGRQMIAIRKRQPEETNNDYETADGGYMTL
FT                                NPRAPTDDDKNIYLTLPPNDHVNSNN -> GPRLRTAAKQS
FT                                SLVGAEVP (in isoform IIC4).
FT                                /FTId=VSP_002644.
FT   VARSPLIC      255   323      NSTDPVKAAQFEPPGRQMIAIRKRQPEETNNDYETADGGYM
FT                                TLNPRAPTDDDKNIYLTLPPNDHVNSNN -> TWTSNDCHQ
FT                                KETT (in isoform IIC3).
FT                                /FTId=VSP_002645.
FT   VARSPLIC      267   323      PPGRQMIAIRKRQPEETNNDYETADGGYMTLNPRAPTDDDK
FT                                NIYLTLPPNDHVNSNN -> MLSCSHLDVK (in
FT                                isoform IIC2).
FT                                /FTId=VSP_002646.
FT   CONFLICT      151   151      R -> K (IN REF. 2; AAC12810).
FT   CONFLICT      164   164      T -> I (IN REF. 2; AAC12809).
SQ   SEQUENCE   323 AA;  35578 MW;  DC4C1A22A0DE4572 CRC64;

  Query Match             26.7%;  Score 371.5;  DB 1;  Length 323;
  Best Local Similarity   37.3%;  Pred. No. 1.8e-23;
  Matches   81;  Conservative   39;  Mismatches   86;  Indels   11;  Gaps    4;

Qy         10 LLCVALLFFAP-DGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNG 68
              ||  |:|| ||  |  | | |  : | | |  : : ::||||| | :  |  | :|||||
Db         29 LLWTAVLFLAPVAGTPAAPPKAVLKLEPQWINVLQEDSVTLTCRGTHSPESDSIQWFHNG 88

Qy         69 SLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPL 128
              :|             |  |||||  ||  | : |:||:| | |:||:||       ||: :
Db         89 NLIPTHTQPSYRFKANNNDSGEYTCQTGQTSLSDPVHLTVLSEWLVLQTPHLEFQEGETI 148

Qy        129 FLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESE 188
              |||| |::  : || ::::|:: |:   : | ||  |    || |:||| :    | |:
Db        149 VLRCHSWKDKPLVKVTFFQNGKSKKFSRSDPNFSIPQANHSHSGDYHCTGNIGYTLYSSK 208

Qy        189 PLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFIS 225
              |: ||| :||          |: :::  || ||: ::

Db        209 PVTITV-QAPSSS-------PMGIIV--AVVTGIAVA 235


Search completed: October  6, 2004, 09:03:36
Job time : 10.6865 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:38 ; Search time 58.1096 Seconds
(without alignments)
1249.617 Million cell updates/sec

Title: US-10-763-400-2
Perfect score: 1390
Sequence: 1 MAPAMESPTLLCVALLFFAP.....RTRKGFRLLNPHPKPNPKNN 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1390	100.0	257	1	AAP90385	Aap90385 Alpha sub
2	1390	100.0	257	2	AAR05025	Aar05025 Alpha sub
3	1390	100.0	257	2	AAR14772	Aar14772 Human Fc(
4	1390	100.0	257	2	AAR42336	Aar42336 Human Fce
5	1390	100.0	257	2	AAW24066	Aaw24066 Alpha sub
6	1390	100.0	257	2	AAW61190	Aaw61190 The alpha
7	1390	100.0	257	4	AAB74667	Aab74667 Human imm
8	1390	100.0	257	4	AAB31584	Aab31584 Amino aci
9	1390	100.0	257	5	ABG32801	Abg32801 Human IgE
10	1390	100.0	257	6	ABO01301	Abo01301 Human pro
11	1390	100.0	257	7	ADD48674	Add48674 Human Pro
12	1390	100.0	260	3	AAY96230	Aay96230 Human Fc
13	1385	99.6	257	2	AAW48094	Aaw48094 Human IgE
14	1377	99.1	257	7	ADB85536	Adb85536 Human imm
15	1264	90.9	232	4	AAB31585	Aab31585 Amino aci
16	1225	88.1	247	2	AAR30483	Aar30483 Human hig
17	1157.5	83.3	218	6	ABO01302	Abo01302 Human pro
18	1117	80.4	978	2	AAW48096	Aaw48096 Human ser
19	1117	80.4	978	5	ABG32803	Abg32803 Human IgE
20	1107.5	79.7	235	2	AAR26064	Aar26064 Human FcE
21	1073	77.2	197	2	AAR45778	Aar45778 Human dih
22	1073	77.2	197	4	AAB31586	Aab31586 A Fc epsi
23	1073	77.2	660	4	AAB31593	Aab31593 Fc epsilo
24	1073	77.2	756	4	AAB31590	Aab31590 Amino aci
25	1039	74.7	193	2	AAR89281	Aar89281 IgE high
26	1008	72.5	183	3	AAY96232	Aay96232 Recombina
27	1006	72.4	182	3	AAY96234	Aay96234 Recombina
28	969	69.7	176	3	AAY94210	Aay94210 Human PhF
29	969	69.7	176	4	AAG65597	Aag65597 Amino aci
30	947	68.1	172	2	AAY33185	Aay33185 Human sFc
31	947	68.1	172	3	AAY94211	Aay94211 Human PhF
32	947	68.1	172	4	AAB31587	Aab31587 A Fc epsi
33	947	68.1	635	4	AAB31594	Aab31594 Fc epsilo
34	947	68.1	731	4	AAB31591	Aab31591 Amino aci
35	944	67.9	176	4	AAG65598	Aag65598 Amino aci
36	832.5	59.9	255	2	AAY27058	Aay27058 Equine Fc
37	799.5	57.5	236	2	AAY27060	Aay27060 Equine Fc
38	775	55.8	281	2	AAR13867	Aar13867 Hybrid Fc
39	705	50.7	253	2	AAW81113	Aaw81113 Canine Fc
40	679	48.8	281	2	AAR13870	Aar13870 Hybrid Fc
41	676	48.6	229	2	AAW81114	Aaw81114 Canine Fc
42	639	46.0	281	2	AAR13872	Aar13872 Fc(gamma)
43	617	44.4	201	2	AAY27061	Aay27061 Recombina
44	606	43.6	281	2	AAR13869	Aar13869 Hybrid Fc
45	597.5	43.0	245	1	AAP90386	Aap90386 Alpha sub

ALIGNMENTS

RESULT 1
AAP90385
ID AAP90385 standard; protein; 257 AA.
XX
AC AAP90385;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX
DE Alpha subunit of human mast cell IgE surface receptor.
XX
KW Immunoglobulin E receptor alpha subunit; allergies;
KW non-peptide drug design; human.
XX
OS Homo sapiens; (Human); mast cell line.
OS KU812.
XX
PN WO8905352-A.
XX
PD 15-JUN-1989.
XX
PF 29-NOV-1988; 88WO-US004255.
XX
PR 01-DEC-1987; 87US-00127214.
XX
PA (HARD) HARVARD COLLEGE.
PA (USSH) NAT INST OF HEALTH.
XX
PI Leder P, Benfey P;
XX
DR WPI; 1989-192698/26.
DR N-PSDB; AAN90126.
XX
PT CDNA encoding IGE receptor alpha-sub-unit - used to treat allergies.
XX
PS Disclosure; Fig 4; 17pp; English.
XX
CC Immunoglobulin E receptor alpha subunit of human mast cell IgE surface
CC recptor (see corresp. AAN90126). Used to produce antibodies which can
CC diagnose IgE receptor levels, measure and treat allergies, and design non
CC -peptide drugs. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
CC 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 257 AA;

Query Match 100.0%; Score 1390; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;

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  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||||||||||
Db        241 KGFRLLNPHPKPNPKNN 257
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```
RESULT 2
AAR05025
ID   AAR05025 standard; protein; 257 AA.
XX
AC   AAR05025;
XX
DT   02-OCT-1990  (first entry)
XX
DE   Alpha subunit of human high affinity IgE receptor.
XX
KW   high affinity IgE receptor; alpha subunit of IgE receptor; human;
KW   allergic response; ss.
XX
OS   Synthetic.
XX
PN   WO9004640-A.
XX
PD   03-MAY-1990.
XX
PF   18-OCT-1988;   88US-00259065.
XX
PR   18-OCT-1988;   88US-00259065.
XX
PA   (USDC ) US SEC OF COMMERCE.
XX
PI   Kinet JP,  Metzger H;
XX
DR   WPI; 1990-164023/21.
DR   N-PSDB; AAQ04644.
XX
PT   DNA sequences for sub-unit peptide(s) of high affinity IgE receptor - and
PT   derived polypeptides, for therapy and diagnosis of allergies, and studies
PT   of IgE receptor interaction.
XX
PS   Disclosure; Page ?; -pp; English.
XX
CC   The high affinity receptor is a tetrameric complex consisting of 2 gamma
CC   subunits and one each of subunits alpha and beta. It is expressed on mast
CC   cells and is involved in the allergic response. COS-7 cells cotransfected
CC   with cDNA for all 3 intact subunit types (derived from rat basophilic
CC   leukaemia cells) express receptor on their surfaces. Detailed study of
CC   the receptors is now possible. See also AAQ04643 and AAQ04645-6
XX
SQ   Sequence 257 AA;

  Query Match             100.0%;  Score 1390;  DB 2;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-103;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||||||||||
Db        241 KGFRLLNPHPKPNPKNN 257
```

```
RESULT 3
AAR14772
ID   AAR14772 standard; protein; 257 AA.
XX
AC   AAR14772;
XX
DT   25-MAR-2003  (revised)
DT   17-DEC-2001  (revised)
DT   03-FEB-1992  (first entry)
XX
DE   Human Fc(epsilon)RI alpha subunit.
XX
KW   Immunoglobulin; receptor; high affinity receptor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /label= signal
FT   Protein         26. .257
FT                   /label= alpha_subunit
FT   Domain          80. .104
FT                   /label= homologous_domain
FT                   /note= "homologous to residues 163-190"
FT   Domain          163. .190
FT                   /label= homologous_domain
FT                   /note= "homologous to residues 80-104"
FT   Region          205. .224
FT                   /label= transmembrane
FT   Region          225. .257
FT                   /label= cytoplasmic
XX
PN   USN7626704-N.
XX
PD   15-OCT-1991.
XX
PF   14-DEC-1990;   90US-00626704.
XX
PR   14-DEC-1990;   90US-00626704.
XX
PA   (USSH ) NAT INST OF HEALTH.
XX
PI   Kinet JP,  Metzger H;
XX
DR   WPI; 1991-346755/47.
DR   N-PSDB; AAQ14736.
XX
PT   DNA coding alpha, beta and gamma-units of ige high affinity receptor -
PT   are used to prepare recombinant polypeptide(s) for treating allergy, drug
PT   screening or monitoring IgE level.
XX
PS   Disclosure; Fig 1; 58pp; English.
XX
```

```
CC   A lambda gt11 library was prepared from poly-A RNA isolated from KUB12
CC   cells. Screening was by a cDNA fragment from the rat Fc(epsilon)RI alpha
CC   cDNA corresponding to nucleotides 119-781. Positive clones were subcloned
CC   and sequenced. This amino acid sequence was deduced from the cDNA clone.
CC   (Note: Revised entry submitted to correct the patent number format of US
CC   Government-owned NTIS applications to prevent clashes with ongoing US
CC   granted patent numbers. For further information please visit the Derwent
CC   web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-
CC   MAR-2003 to correct PF field.)
XX
SQ   Sequence 257 AA;

  Query Match             100.0%;  Score 1390;  DB 2;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-103;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||||||||||
Db        241 KGFRLLNPHPKPNPKNN 257


RESULT 4
AAR42336
ID   AAR42336 standard; protein; 257 AA.
XX
AC   AAR42336;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1994  (first entry)
XX
DE   Human FceRI alpha.
XX
KW   IgE; immunoglogulin E receptor; beta subunit; basophils; allergy;
KW   aggregation; signal transduction; diagnosis; antagonist.
XX
OS   Homo sapiens.
XX
PN   WO9321317-A1.
XX
PD   28-OCT-1993.
XX
PF   16-APR-1993;   93WO-US003419.
XX
PR   16-APR-1992;   92US-00869933.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX
PI   Kinet JP;
XX
DR   WPI; 1993-351727/44.
DR   N-PSDB; AAQ51020.
XX
PT   Immunoglobulin E receptor human beta sub-unit isolation - using 1st
PT   strand reverse transcripts from human basophils as templates for a
PT   polymerase chain reaction, used to treat and diagnose allergic diseases.
XX
PS   Claim 5; Fig 1; 154pp; English.
XX
CC   The sequence is that of the human FcRI alpha subunit, isolated by using
CC   first strand reverse transcriptase from human basophils by PCR. The gene
CC   and its prod. can be used to identify human beta subuit FceRI inhibitors
CC   (immunoglobulin E receptor) which inhibit the binding of IgE to its
CC   receptor and inhibit the aggragation function of the receptor or the
CC   signal transducing function related to allergic response. Such inhibitors
CC   can be used for the treatment or prevention of allergic disease. See also
CC   AAR42337-42. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 257 AA;

  Query Match             100.0%;  Score 1390;  DB 2;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-103;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||||||||||
Db        241 KGFRLLNPHPKPNPKNN 257


RESULT 5
AAW24066
ID   AAW24066 standard; protein; 257 AA.
XX
AC   AAW24066;
XX
DT   04-FEB-1998  (first entry)
XX
DE   Alpha subunit of human high affinity receptor for IgE (human FcERI).
XX
KW   alpha subunit; human high affinity receptor; IgE; FcERI; antigen;
KW   preformed mediator; histamine; serotonin; leukotriene; IgE level;
KW   allergic condition; therapy; allergic response; drug screening;
KW   DNA probe; diagnostic assay.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /label= signal_peptide
FT   Protein         26. .257
FT                   /label= mature_peptide
FT   Region          26. .204
FT                   /label= extracellular_portion_of_protein
FT   Domain          80. .104
FT                   /label= homologous_domain_1
FT                   /note= "this region is homologous with amino acids 163-
FT                   190"
FT   Domain          163. .190
FT                   /label= homologous_domain_2
FT                   /note= "this region is homologous with amino acids 80-
FT                   104"
FT   Region          205. .224
FT                   /label= transmembrane_segment
FT   Region          225. .257
FT                   /label= cytoplasmic_domain
```

XX
PN US5639660-A.
XX
PD 17-JUN-1997.
XX
PF 24-FEB-1988; 88US-00160457.
XX
PR 24-FEB-1988; 88US-00160457.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (HOFF) HOFFMANN LA ROCHE INC.
XX
PI Kochan JP, Kinet JP;
XX
DR WPI; 1997-332052/30.
DR N-PSDB; AAT85615.
XX
PT DNA encoding alpha sub-unit of high affinity receptor for immunoglobulin
PT E - used for producing polypeptide(s) which can be used for therapy or to
PT prevent allergic responses or in diagnostic and screening assays.
XX
PS Claim 7; Fig 1A-B; 15pp; English.
XX
CC This sequence represents the alpha subunit of the human high affinity
CC receptor for IgE (FcERI). FcERI is found exclusively on mast cells,
CC basophils and related cells. Aggregation of IgE occupied FcERI by antigen
CC triggers both the release of of preformed mediators such as histamine and
CC serotonin, as well as stimulating the synthesis of leukotrienes. It is
CC the release of these mediators that results in an allergic condition. The
CC DNA can be used to produce the human FcERI alpha polypeptides which can
CC be used for therapy or to prevent allergic responses, in drug screening
CC assays or for monitoring IgE levels in patients. The DNA encoding this
CC protein can also be used to produce DNA probes useful in diagnostic
CC assays
XX
SQ Sequence 257 AA;

Query Match 100.0%; Score 1390; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||||||||||
Db        241 KGFRLLNPHPKPNPKNN 257
```

RESULT 6
AAW61190
ID AAW61190 standard; protein; 257 AA.
XX
AC AAW61190;
XX
DT 07-OCT-1998 (first entry)
XX
DE The alpha chain of a Fc epsilon receptor.
XX
KW Alpha chain; human; Fc epsilon receptor; canine; equine; feline;
KW immunoglobulin E; IgE; detection; diagnose; allergy; atopic disease;
KW hyper-IgE syndrome; internal parasitic infection; B cell neoplasia;
KW flea allergy; heartworm infection.
XX
OS Homo sapiens.
XX
PN WO9823964-A1.
XX
PD 04-JUN-1998.
XX
PF 24-NOV-1997; 97WO-US021651.
XX
PR 26-NOV-1996; 96US-00756387.
XX
PA (HESK-) HESKA CORP.
XX
PI Frank RG, Porter JP, Rushlow KE, Wassom DL;
XX
DR WPI; 1998-322873/28.
DR N-PSDB; AAV36343.
XX
PT Detection of non-human immunoglobulin E - by complex formation with human
PT Fc epsilon receptor, used for, e.g. diagnosis of allergy and atopic
PT disease.
XX
PS Disclosure; Page 37-38; 70pp; English.
XX
CC The present sequence represents the alpha chain of the human Fc epsilon
CC receptor. Detection of canine, equine or feline immunoglobulin E (IgE)
CC comprises reacting isolated human Fc epsilon receptor with the test
CC sample and detecting formation of a IgE-receptor complex. Detection of
CC IgE is used to diagnose allergy, atopic disease, hyper-IgE syndrome,
CC internal parasitic infections or B cell neoplasia, and for measuring
CC effect of treatments. Most particularly flea allergy in dogs and cats is
CC detected, and also heartworm infection
XX
SQ Sequence 257 AA;

Query Match 100.0%; Score 1390; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||||||||||
Db        241 KGFRLLNPHPKPNPKNN 257
```

RESULT 7
AAB74667
ID AAB74667 standard; protein; 257 AA.
XX
AC AAB74667;
XX
DT 19-JUN-2001 (first entry)
XX
DE Human immunoglobulin E receptor I alpha subunit protein.
XX

KW Human; polymorphism; immunoglobulin E receptor I alpha subunit; IGERA;
KW single nucleotide polymorphism; SNP; allele specific oligonucleotide;
KW immunoassay; detection.
XX
OS Homo sapiens.
XX
PN WO200111010-A2.
XX
PD 15-FEB-2001.
XX
PF 02-AUG-2000; 2000WO-US021097.
XX
PR 09-AUG-1999; 99US-0147860P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Denton RR, Duda A, Kliem SE, Lanz EM, Nandabalan K;
PI Stephens JC;
XX
DR WPI; 2001-202766/20.
DR N-PSDB; AAF97964.
XX
PT New polynucleotide for gene therapy, comprises nucleotide polymorphisms
PT in the immunoglobulin E receptor I alpha subunit gene.
XX
PS Claim 10; Fig 3; 99pp; English.
XX
CC The present invention describes an isolated polynucleotide (I) comprising
CC a nucleotide sequence (S) which is a polymorphic variant of a reference
CC sequence for the human immunoglobulin E receptor I alpha subunit (IGERA)
CC gene or its fragment. The polymorphic variant comprises at least one
CC polymorphism selected from guanine (G) at polymorphic site (PS) 1, PS9,
CC PS10 or PS21, cytosine (C) at PS2, PS3, PS6, PS12, PS18 or PS20, adenine
CC (A) at PS5, PS7, PS11, PS13, PS14, PS15, PS19, or PS22 and thymine (T) at
CC PS4, PS8, PS16 or PS17, or (G) at a position corresponding to nucleotide
CC 251, (A) at a position corresponding to nucleotide 302 or 741, and (T) at
CC a position corresponding to nucleotide 530. (I) can be used in gene
CC therapy. (I) is useful for therapeutic purposes. A polypeptide (II)
CC encoded by (I) is useful in drug screening assays and in assays to
CC measure the binding affinity of one or more candidate drugs targeting
CC (II). An antibody (III) to (II) is useful to immunoprecipitate (II) from
CC solution and also reacts with (II) on Western or immunoblots of
CC polyacrylamide gels on membrane supports or substrates. (III) is also
CC useful in immunoassays to detect (II) in biological samples. AAF97965 to
CC AAF98096 represent IGERA allele specific oligonucleotide probes; AAF98097
CC to AAF98140 represent IGERA gene polymorphism detection primers; and
CC AAF98141 to AAF98180 represent IGERA gene PCR primers which are used in
CC the exemplification of the present invention. The present sequence
CC represents the human IGERA protein used in the present invention
XX
SQ Sequence 257 AA;

Query Match 100.0%; Score 1390; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||||||||||
Db        241 KGFRLLNPHPKPNPKNN 257
```

RESULT 8
AAB31584
ID AAB31584 standard; protein; 257 AA.
XX
AC AAB31584;
XX
DT 30-APR-2001 (first entry)
XX
DE Amino acid sequence of a human Fc epsilon receptor alpha-chain.
XX
KW Fc epsilon receptor; FcepsilonR; immunoglobulin E; IgE; atopic disease;
KW luminescence inducing protein; allergy; hyper IgE syndrome;
KW internal parasite infection; B cell neoplasia.
XX
OS Homo sapiens.
XX
PN WO200104310-A1.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US019070.
XX
PR 13-JUL-1999; 99US-0143612P.
PR 02-MAR-2000; 2000US-0186412P.
XX
PA (HESK-) HESKA CORP.
PA (PROM-) PROMEGA CORP.
XX
PI Weber ER, Wood KV, Hall MP;
XX
DR WPI; 2001-103082/11.
DR N-PSDB; AAF24911.
XX
PT A fusion protein, comprising an Fc epsilon receptor domain and a
PT luminescence inducing protein domain that induces a LP substrate to emit
PT light when contacted with the LP domain, useful for detecting
PT immunoglobulin (Ig) E.
XX
PS Claim 16; Page 60; 105pp; English.
XX
CC The present sequence represents a human Fc epsilon receptor (FcepsilonR)
CC alpha-chain protein, that binds to immunoglobulin (Ig) E). The FcepsilonR
CC domain is used to produce a fusion protein, which also comprises a
CC luminescence inducing protein domain that induces a substrate to emit
CC light when contacted with the luminescence inducing protein domain. The
CC fusion protein may be used to detect IgE. It may also be used to identify
CC a compound capable of inhibiting FcepsilonR protein activity. IgE
CC antibody production is indicative of diseases such as allergies, atopic
CC disease, hyper IgE syndrome, internal parasite infections and B cell
CC neoplasia. Detection of IgE production in an animal following therapy is
CC indicative of the efficacy of the treatment, for example when using
CC treatments intended to disrupt IgE production
XX
SQ Sequence 257 AA;

Query Match 100.0%; Score 1390; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||||||||||
Db        241 KGFRLLNPHPKPNPKNN 257
```

```
RESULT 9
ABG32801
ID   ABG32801 standard; protein; 257 AA.
XX
AC   ABG32801;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human IgE receptor FcepsilonRIalpha.
XX
KW   Human; IgE; receptor; FcepsilonRIalpha; HSA; human serum albumin;
KW   antiallergic; dermatological; antiinflammatory; antiasthmatic;
KW   IgE binding domain; systemic allergy; IgE-receptor-mediated disorder;
KW   atopic dermatitis; atopic asthma; chronic urticaria.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /label= Signal_peptide
FT   Protein         26. .257
FT                   /label= Mature_FcepsilonRIalpha
FT   Region          26. .204
FT                   /label= IgE_binding_domain
FT                   /note= "This region is specifically claimed in claim 5"
XX
PN   US6423512-B1.
XX
PD   23-JUL-2002.
XX
PF   21-JUL-1997;   97US-00897956.
XX
PR   26-JUL-1996;   96US-0022689P.
XX
PA   (NOVS ) NOVARTIS AG.
XX
PI   Digan ME,  Lake P,  Gram H;
XX
DR   WPI; 2002-672940/72.
DR   N-PSDB; ABS52959.
XX
PT   New fusion IgE-binding polypeptide, useful for the prevention and
PT   treatment of systemic allergy and/or other IgE-receptor-mediated
PT   disorders such as atopic dermatitis, atopic asthma and chronic urticaria.
XX
PS   Claim 5; Fig 13; 49pp; English.
XX
CC   The invention relates to a new fusion polypeptide or its pharmaceutically
CC   acceptable salt comprises at least one IgE-binding domain fused to at
CC   least one human serum albumin (HSA) component, where the IgE-binding
CC   domain is the sequence (a) defined residues Val26-Leu204 of the protein
CC   sequence appearing as ABG32801, or a truncation at the carboxy terminus
CC   by 1-12 amino acids. Also included are: (1) a fusion polypeptide defined
CC   by residues Val26-Leu978 of the protein appearing as ABG32803; (2) a
CC   polynucleotide sequence encoding the fusion protein; (3) a host cell
CC   transformed with the polynucleotide; (4) a method of preparing the fusion
CC   protein comprising transforming a host cell with a vector comprising a
CC   polynucleotide encoding the fusion polypeptide, expressing the fusion
CC   polypeptide in the cell, and recovering the fusion polypeptide from the
CC   host cell, optionally in the form of its salt; and (5) a vector for
CC   expressing a polynucleotide sequence encoding a fusion polypeptide of
CC   formula (I), (II), (III), (IV), or (V) or its salts ( R_1-L-R_2 (I), R_2-
CC   L-R_1 (II), R_1-L-R_2-L-R_1 (III), R_1-L-R_1-L-R_2 (IV), R_2-L-R_1-L-R_1
CC   (V), where R_1 = the polypeptide (a) or its truncation at the carboxy
CC   terminus by 1-12 amino acids and R_2 = a polypeptide selected from the
CC   sequence defined by residues Asp25-Leu609 the human HSA sequence
CC   appearing as ABG32802, or its truncation at the carboxy terminus by 1-10
CC   amino acids and L = independently a chemical bond, where the vector is
CC   PXMT3-R1a-HAS-R1a). The compositions and methods of the present invention
CC   are useful for the prevention and treatment of systemic allergy and other
CC   IgE-receptor-mediated disorders such as atopic dermatitis, atopic asthma
CC   and chronic urticaria. The IgE-binding polypeptide have a more prolonged
CC   effective serum life, more improved clinical utility in the treatment of
CC   allergy, as well as improved activity in a more efficient and cost-
CC   effective manner. The present sequence is the human IgE receptor
CC   FcepsilonRIalpha used to make the fusion protein of the invention
XX
SQ   Sequence 257 AA;
```

```
  Query Match             100.0%;  Score 1390;  DB 5;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-103;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||||||||||
Db        241 KGFRLLNPHPKPNPKNN 257
```

```
RESULT 10
ABO01301
ID   ABO01301 standard; protein; 257 AA.
XX
AC   ABO01301;
XX
DT   07-AUG-2003  (first entry)
XX
DE   Human protein NOV8a.
XX
KW   Human; NOVX; cardiomyopathy; atherosclerosis; hypertension;
KW   congenital heart defect; prostate cancer; diabetes; metabolic disorder;
KW   neoplasm; graft versus host disease; AIDS; bronchial asthma;
KW   Crohn's disease; multiple sclerosis; infectious disease; anorexia;
KW   cancer-associated cachexia; neurodegenerative disorder;
KW   Alzheimer's disease; Parkinson's disease; immune disorder;
KW   haematopoietic disorder; dyslipidaemia; wasting disorder; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003023008-A2.
XX
PD   20-MAR-2003.
XX
PF   09-SEP-2002; 2002WO-US028596.
XX
PR   07-SEP-2001; 2001US-0318120P.
PR   07-SEP-2001; 2001US-0318130P.
PR   10-SEP-2001; 2001US-0318430P.
PR   12-SEP-2001; 2001US-0318765P.
PR   17-SEP-2001; 2001US-0322781P.
```

PR 17-SEP-2001; 2001US-0322816P.
PR 19-SEP-2001; 2001US-0323519P.
PR 20-SEP-2001; 2001US-0323631P.
PR 20-SEP-2001; 2001US-0323636P.
PR 25-SEP-2001; 2001US-0324969P.
PR 25-SEP-2001; 2001US-0325091P.
PR 26-SEP-2001; 2001US-0324990P.
PR 15-FEB-2002; 2002US-0357303P.
PR 28-FEB-2002; 2002US-0360973P.
PR 20-MAR-2002; 2002US-0366131P.
PR 25-MAR-2002; 2002US-0367753P.
PR 02-APR-2002; 2002US-0369479P.
PR 10-MAY-2002; 2002US-0379532P.
PR 17-MAY-2002; 2002US-0381664P.
PR 17-MAY-2002; 2002US-0381672P.
PR 28-MAY-2002; 2002US-0383651P.
PR 29-MAY-2002; 2002US-0384012P.
PR 19-JUN-2002; 2002US-0390155P.
PR 06-SEP-2002; 2002US-00390155.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Zhong M, Li L, Gorman L, Spytek KA, Kekuda R, Taupier RJ;
PI Anderson DW, Vernet CAM, Catterton E, Miller CE, Shenoy SG;
PI Patturajan M, Pena CEA, Tchernev VT, Padigaru M, Gusev VY;
PI Malyankar UM, Burgess CE, Gerlach VL, Casman SJ, Rieger DK;
PI Grosse WM, Smithson G, Peyman JA, Starling G, Rothenberg ME;
PI Larochelle WJ, Shimkets RA, Crabtree J, Rastelli L, Voss EZ;
PI Boldog FL, Edinger SR, Millet I, Macdougall JR, Ellerman K;
PI Chapoval A;
XX
DR WPI; 2003-313246/30.
DR N-PSDB; ACD06182.
XX
PT New polypeptides and polynucleotides having properties related to
PT stimulation of biochemical or physiological responses in a cell or
PT tissue, useful for diagnosing or preventing e.g. atherosclerosis,
PT hypertension, prostate cancer.
XX
PS Claim 2; Page 133; 849pp; English.
XX
CC The invention relates to an isolated polypeptide comprising one of 127
CC sequences (appearing as ABO1288-ABO1414) designated as NOVX, a mature
CC form of NOVX, an amino acid sequence which is at least 95% identical to
CC NOVX or an amino acid sequence comprising one or more conservative
CC substitutions in NOVX. Also included are nucleic acids encoding NOVX
CC proteins, determining the presence or amount of NOVX or NOVX DNA in a
CC sample (by introducing the sample to an antibody that binds
CC immunospecifically to the polypeptide, and determining the presence or
CC amount of antibody bound to the polypeptide), determining the presence of
CC or predisposition to a disease associated with altered levels of
CC expression of NOVX or NOVX DNA in a first mammalian subject, identifying
CC an agent that binds to NOVX, identifying a potential therapeutic agent
CC for treatment of a pathology related to aberrant expression or aberrant
CC physiological interactions of NOVX, screening for a modulator of activity
CC of or of latency or predisposition to a pathology associated with NOVX, a
CC vector comprising NOVX DNA, a cell comprising the vector (used to produce
CC NOVX) and an anti-NOVX antibody. The NOVX nucleic acids and polypeptides
CC are useful as a marker for cell or tissue type, and in diagnosing and
CC treating pathologies, diseases, conditions or disorders associated with
CC NOVX sequences, including cardiomyopathy, atherosclerosis, hypertension,
CC congenital heart defects, prostate cancer, diabetes, metabolic disorders,
CC neoplasm, graft versus host disease, AIDS, bronchial asthma, Crohn's
CC disease, multiple sclerosis, infectious diseases, anorexia, cancer-
CC associated cachexia, neurodegenerative disorders (e.g. Alzheimer's
CC disease or Parkinson's disease), immune disorders, haematopoietic
CC disorders, dyslipidaemias, and wasting disorders associated with chronic
CC diseases. These may also be used to screen for molecules which inhibit or
CC enhance NOVX activity or function, and for detecting specific cell types.
CC These may also be used in chromosome mapping, gene therapy, tissue
CC typing, and in forensic biology. The present sequence represents a NOVX
CC protein
XX

SQ Sequence 257 AA;

Query Match 100.0%; Score 1390; DB 6; Length 257;
Best Local Similarity 100.0%; Pred. No. 3.3e-103;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||||||||||
Db        241 KGFRLLNPHPKPNPKNN 257
```

RESULT 11
ADD48674
ID ADD48674 standard; protein; 257 AA.
XX
AC ADD48674;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P12319, SEQ ID NO 14381.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P12319.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent

```
CC   that increases or decreases the expression of the polynucleotide sequence
CC   that is differentially expressed in neuronal tissue of a first animal
CC   subjected to pain, a method for identifying a compound which regulates
CC   the expression of a polynucleotide sequence which is differentially
CC   expressed in an animal subjected to pain, a method for identifying a
CC   compound that regulates the activity of one or more of the
CC   polynucleotides, a method for producing a pharmaceutical composition, a
CC   method for identifying a compound or small molecule that regulates the
CC   activity in an animal of one or more of the polypeptides given in the
CC   specification, a method for identifying a compound useful in treating
CC   pain and a pharmaceutical composition comprising the one or more
CC   polypeptides or their antibodies. The polynucleotide or the compound that
CC   modulates its activity is useful for preparing a medicament for treating
CC   pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC   injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC   therapy). The sequence presented is a human protein (shown in Table 2 of
CC   the specification) which is differentially expressed during pain. Note:
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic form directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 257 AA;

  Query Match             100.0%;  Score 1390;  DB 7;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 3.3e-103;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||||||||||
Db        241 KGFRLLNPHPKPNPKNN 257


RESULT 12
AAY96230
ID   AAY96230 standard; protein; 260 AA.
XX
AC   AAY96230;
XX
DT   11-SEP-2000  (first entry)
XX
DE   Human Fc receptor, FcepsilonRIa.
XX
KW   Human; Fc receptor; FcepsilonRIa; immunoglobulin; infection;
KW   immune response; HIV; IgG; immunosuppressive; antirheumatic;
KW   antiinflammatory; AIDS; SLE; multiple myeloma; rheumatoid arthritis;
KW   systemic lupus erythematosus; tumour.
XX
OS   Homo sapiens.
XX
PN   EP1006183-A1.
XX
PD   07-JUN-2000.
XX
PF   03-DEC-1998;   98EP-00122969.
XX
PR   03-DEC-1998;   98EP-00122969.
XX
PA   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
DR   WPI; 2000-367968/32.
DR   N-PSDB; AAA27470.
XX
PT   Novel Fc receptor lacking transmembrane domains, a signal peptide, and
PT   glycosylation, useful for diagnosing and treating immune disorders and
PT   cancer.
XX
PS   Disclosure; Page 40-41; 60pp; English.
XX
CC   The present sequence is the human Fc receptor, FcepsilonRIa. Fc receptors
CC   play an important role in defending the body against infections. First,
CC   pathogens are opsonised by serum immunoglobulins. The resulting complex
CC   then binds to cells expressing Fc receptors. Upon Fc receptor activation,
CC   immune effector pathways are activated, leading to immune response. The
CC   present sequence may be modified to produce recombinant versions. The
CC   recombinant Fc receptor consist only of the extracellular portion of the
CC   receptor and are not glycosylated i.e. they do not have transmembrane
CC   domains or signal peptides. The recombinant proteins may be used in
CC   immunoassays to determine the immune status of patients with chronic
CC   diseases of the immune system, e.g. AIDS, systemic lupus erythematosus
CC   (SLE), multiple myeloma (MM), or rheumatoid arthritis. In addition,
CC   pharmaceutical compositions containing recombinant proteins may be used
CC   to treat or prevent autoimmune diseases, allergies or tumours, especially
CC   AIDS, rheumatoid arthritis or MM
XX
SQ   Sequence 260 AA;

  Query Match             100.0%;  Score 1390;  DB 3;  Length 260;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-103;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 63

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 123

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 183

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 243

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||||||||||
Db        244 KGFRLLNPHPKPNPKNN 260


RESULT 13
AAW48094
ID   AAW48094 standard; protein; 257 AA.
XX
AC   AAW48094;
XX
DT   20-JUL-1998  (first entry)
XX
DE   Human IgE receptor Fc-epsilon-RI alpha chain.
XX
KW   Fc-epsilon RI alpha chain; IgE receptor; human serum albumin;
KW   fusion protein; allergy; atopic dermatitis; asthma; urticaria; hay fever;
KW   eczema; anaphylaxis; gene therapy; diagnosis; transgenic animal.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /label= Sig_peptide
```

```
FT   Protein         26. .257
FT                   /label= Mat_protein
FT   Domain          26. .204
FT                   /note= "extracellular domain"
XX
PN   WO9804718-A1.
XX
PD   05-FEB-1998.
XX
PF   25-JUL-1997;   97WO-EP004066.
XX
PR   26-JUL-1996;   96US-00690216.
XX
PA   (NOVS ) NOVARTIS AG.
XX
PI   Digan ME,  Lake P,  Gram H;
XX
DR   WPI; 1998-130705/12.
DR   N-PSDB; AAV20402.
XX
PT   New fusion polypeptide for, e.g. diagnosing allergies - comprises
PT   immunoglobulin E-binding domain fused to human serum albumin.
XX
PS   Claim 2; Page 44; 77pp; English.
XX
CC   This is the amino acid sequence of the dominant form of full-length
CC   native human IgE receptor Fc-epsilon RI alpha chain. A claimed fusion
CC   protein (FP) comprises an IgE binding domain fused to at least one human
CC   serum albumin (HSA) component (see AAW38095), optionally via a peptide
CC   linker, and is especially a dimeric FP (see AAW48096) comprising HSA
CC   fused, at each of its N- and C-termini, to the extracellular domain of Fc
CC   -epsilon RI alpha chain. Also claimed are: nucleic acids encoding the FP
CC   (see AAV20404); a vector; a process for preparing the FP; a method of
CC   performing gene therapy in humans that comprises removing somatic cells
CC   from a patient, genetically modifying them in culture by insertion of a
CC   polynucleotide that encodes the FP, and reintroducing the modified cells
CC   into the patient so that the FP is expressed by the cells of the patient;
CC   and use of the FP in an in vitro diagnostic assay to determine the level
CC   of IgE or auto-antibodies to Fc epsilon RI in a sample. The products can
CC   be used in the prevention and/or treatment of IgE-mediated allergic
CC   diseases and related disorders such as atopic dermatitis, atopic asthma,
CC   chronic urticaria, hayfever and eczema. Compared with using IgE binding
CC   domain alone, the FP has a longer serum life, and thus greater activity,
CC   without a loss of ability to bind serum IgE or circulating auto-
CC   antibodies
XX
SQ   Sequence 257 AA;

  Query Match             99.6%;  Score 1385;  DB 2;  Length 257;
  Best Local Similarity   99.6%;  Pred. No. 8.3e-103;
  Matches  256;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||| ||||||
Db        241 KGFRLLNPHPNPNPKNN 257
```

```
RESULT 14
ADB85536
ID   ADB85536 standard; protein; 257 AA.
XX
AC   ADB85536;
XX
DT   04-DEC-2003  (first entry)
XX
DE   Human immunoglobulin E high affinity receptor alpha subunit protein.
XX
KW   alpha subunit; high affinity receptor for immunoglobulin E; FcERI;
KW   mast cell; basophil; histamine; serotonin; allergic condition;
KW   antiallergic; allergic response; drug screening assay; immunoglobulin E;
KW   human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 221
FT                   /note= "Encoded by GGA"
FT   Misc-difference 253
FT                   /note= "Encoded by AAC"
XX
PN   US6602983-B1.
XX
PD   05-AUG-2003.
XX
PF   22-SEP-1994;   94US-00310902.
XX
PR   24-FEB-1988;   88US-00160457.
PR   30-OCT-1991;   91US-00785127.
PR   29-MAY-1993;   93US-00066640.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Kinet JP,  Kochan JP;
XX
DR   WPI; 2003-669612/63.
DR   N-PSDB; ADB85535.
XX
PT   New alpha subunit of the human high affinity receptor for immunoglobulin
PT   E polypeptides, useful as antagonists to prevent allergic response, as
PT   reagents in drug screening assays, or for monitoring immunoglobulin E
PT   levels in patients.
XX
PS   Claim 1; Fig 1; 9pp; English.
XX
CC   This invention relates to a novel purified polypeptide corresponding to
CC   the alpha subunit of the human high affinity receptor for immunoglobulin
CC   E (FcERI) and the DNA sequence which encodes it. The receptor of the
CC   invention is found exclusively on mast cells, basophils and related
CC   cells. Activation of the receptor triggers the release of preformed
CC   mediators such as histamine and serotonin which may result in allergic
CC   conditions. Compounds which modulate FcERI activity may have antiallergic
CC   activity. The polypeptide of the invention may be useful as an antagonist
CC   for preventing allergic response, as a reagent in drug screening assays,
CC   as a therapeutic or for monitoring immunoglobulin E levels in patients.
CC   The DNA sequences may be useful for producing the polypeptide or for
CC   synthesising cDNA sequences to construct DNA probes used in diagnostic
CC   assays. The present sequence is the amino acid sequence of the alpha
CC   subunit of the human FcERI receptor of the invention.
XX
SQ   Sequence 257 AA;

  Query Match             99.1%;  Score 1377;  DB 7;  Length 257;
  Best Local Similarity   99.2%;  Pred. No. 3.6e-102;
  Matches  255;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
```

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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTELFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
                 |||||||||||||:||||
Db        241 KGFRLLNPHPKPDPKNN 257
```

RESULT 15
AAB31585
ID AAB31585 standard; protein; 232 AA.
XX
AC AAB31585;
XX
DT 30-APR-2001 (first entry)
XX
DE Amino acid sequence of Fc epsilon receptor alpha-chain mature protein.
XX
KW Fc epsilon receptor; FcepsilonR; immunoglobulin E; IgE; atopic disease;
KW luminescence inducing protein; allergy; hyper IgE syndrome;
KW internal parasite infection; B cell neoplasia.
XX
OS Homo sapiens.
XX
PN WO200104310-A1.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US019070.
XX
PR 13-JUL-1999; 99US-0143612P.
PR 02-MAR-2000; 2000US-0186412P.
XX
PA (HESK-) HESKA CORP.
PA (PROM-) PROMEGA CORP.
XX
PI Weber ER, Wood KV, Hall MP;
XX
DR WPI; 2001-103082/11.
DR N-PSDB; AAF24913.
XX
PT A fusion protein, comprising an Fc epsilon receptor domain and a
PT luminescence inducing protein domain that induces a LP substrate to emit
PT light when contacted with the LP domain, useful for detecting
PT immunoglobulin (Ig) E.
XX
PS Claim 16; Page 62-63; 105pp; English.
XX
CC The present sequence represents a human Fc epsilon receptor (FcepsilonR)
CC alpha-chain mature protein, that binds to immunoglobulin (Ig) E). The
CC FcepsilonR domain is used to produce a fusion protein, which also
CC comprises a luminescence inducing protein domain that induces a substrate
CC to emit light when contacted with the luminescence inducing protein
CC domain. The fusion protein may be used to detect IgE. It may also be used
CC to identify a compound capable of inhibiting FcepsilonR protein activity.
CC IgE antibody production is indicative of diseases such as allergies,
CC atopic disease, hyper IgE syndrome, internal parasite infections and B
CC cell neoplasia. Detection of IgE production in an animal following
CC therapy is indicative of the efficacy of the treatment, for example when
CC using treatments intended to disrupt IgE production
XX
SQ Sequence 232 AA;

Query Match 90.9%; Score 1264; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 3.6e-93;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60

Qy         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145
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Db         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120

Qy        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205
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Db        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180

Qy        206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
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Search completed: October 6, 2004, 09:03:04
Job time : 62.1096 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:40 ; Search time 16.7739 Seconds
(without alignments)
790.984 Million cell updates/sec

Title: US-10-763-400-2
Perfect score: 1390
Sequence: 1 MAPAMESPTLLCVALLFFAP.....RTRKGFRLLNPHPKPNPKNN 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1390	100.0	257	1	US-07-869-933-11	Sequence 11, Appl
2	1390	100.0	257	2	US-08-756-387B-2	Sequence 2, Appli
3	1390	100.0	257	3	US-09-103-663-11	Sequence 11, Appl
4	1390	100.0	257	4	US-09-285-873-2	Sequence 2, Appli
5	1390	100.0	257	4	US-08-897-956A-1	Sequence 1, Appli
6	1390	100.0	257	4	US-09-944-277A-2	Sequence 2, Appli
7	1264	90.9	232	1	US-07-869-933-13	Sequence 13, Appl
8	1264	90.9	232	2	US-08-756-387B-6	Sequence 6, Appli
9	1264	90.9	232	3	US-09-103-663-13	Sequence 13, Appl
10	1264	90.9	232	4	US-09-285-873-6	Sequence 6, Appli
11	1264	90.9	232	4	US-09-944-277A-6	Sequence 6, Appli
12	1117	80.4	978	4	US-08-897-956A-3	Sequence 3, Appli
13	1073	77.2	197	2	US-08-756-387B-11	Sequence 11, Appl
14	1073	77.2	197	4	US-09-285-873-11	Sequence 11, Appl
15	1073	77.2	197	4	US-09-944-277A-11	Sequence 11, Appl
16	1067	76.8	197	3	US-08-788-954-2	Sequence 2, Appli
17	1039	74.7	193	2	US-08-765-536-1	Sequence 1, Appli
18	1039	74.7	193	5	PCT-US95-08401-1	Sequence 1, Appli
19	947	68.1	172	2	US-08-756-387B-13	Sequence 13, Appl
20	947	68.1	172	4	US-09-285-873-13	Sequence 13, Appl
21	947	68.1	172	4	US-09-245-764-9	Sequence 9, Appli
22	947	68.1	172	4	US-09-944-277A-13	Sequence 13, Appl
23	832.5	59.9	255	3	US-09-015-734-2	Sequence 2, Appli
24	832.5	59.9	255	4	US-09-515-311-2	Sequence 2, Appli
25	799.5	57.5	236	3	US-09-015-734-7	Sequence 7, Appli
26	799.5	57.5	236	4	US-09-515-311-7	Sequence 7, Appli
27	722	51.9	263	2	US-08-768-964-2	Sequence 2, Appli
28	722	51.9	263	3	US-09-005-299-2	Sequence 2, Appli
29	722	51.9	263	3	US-09-515-431-2	Sequence 2, Appli
30	705	50.7	253	3	US-08-833-488B-20	Sequence 20, Appl
31	690.5	49.7	238	2	US-08-768-964-7	Sequence 7, Appli
32	690.5	49.7	238	3	US-09-005-299-7	Sequence 7, Appli
33	690.5	49.7	238	3	US-09-515-431-7	Sequence 7, Appli
34	676	48.6	229	3	US-08-833-488B-24	Sequence 24, Appl
35	617	44.4	201	3	US-09-015-734-12	Sequence 12, Appl
36	617	44.4	201	4	US-09-515-311-12	Sequence 12, Appl
37	587.5	42.3	227	1	US-07-869-933-14	Sequence 14, Appl
38	587.5	42.3	227	3	US-09-103-663-14	Sequence 14, Appl
39	576.5	41.5	222	1	US-07-869-933-12	Sequence 12, Appl
40	576.5	41.5	222	1	US-07-869-933-28	Sequence 28, Appl
41	576.5	41.5	222	3	US-09-103-663-12	Sequence 12, Appl
42	576.5	41.5	222	3	US-09-103-663-28	Sequence 28, Appl
43	554	39.9	199	3	US-08-833-488B-14	Sequence 14, Appl
44	546	39.3	431	4	US-09-592-998C-9	Sequence 9, Appli
45	546	39.3	435	4	US-09-592-998C-10	Sequence 10, Appl

ALIGNMENTS

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RESULT 1
US-07-869-933-11
; Sequence 11, Application US/07869933
; Patent No. 5770396
;  GENERAL INFORMATION:
;    APPLICANT:  KINET, Jean-Pierre
;    TITLE OF INVENTION:  ISOLATION, CHARACTERIZATION, AND USE OF
;    TITLE OF INVENTION:  THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
;    TITLE OF INVENTION:  IMMUNOGLOBULIN
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/869,933
;      FILING DATE:  19920416
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  40399/154 NIHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  257 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-869-933-11

  Query Match           100.0%;  Score 1390;  DB 1;  Length 257;
  Best Local Similarity  100.0%;  Pred. No. 6.1e-127;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
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Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
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Qy          61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
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Db          61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy         121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
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Db         121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy         181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
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Db         181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy         241 KGFRLLNPHPKPNPKNN 257
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Db         241 KGFRLLNPHPKPNPKNN 257
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RESULT 2
US-08-756-387B-2
; Sequence 2, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-756-387B-2

Query Match 100.0%; Score 1390; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 6.1e-127;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db           1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy          61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
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Qy         121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
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Db         121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy         181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
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Db         181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy         241 KGFRLLNPHPKPNPKNN 257
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Db         241 KGFRLLNPHPKPNPKNN 257
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RESULT 3
US-09-103-663-11
; Sequence 11, Application US/09103663D
; Patent No. 6171803.
; GENERAL INFORMATION:
; APPLICANT: Kinet et al.
; TITLE OF INVENTION: Isolation, characterization, and use of the human beta
; TITLE OF INVENTION: subunit of the high affinity receptor for
; TITLE OF INVENTION: immunoglobulin E.
; FILE REFERENCE: 50490
; CURRENT APPLICATION NUMBER: US/09/103,663D
; CURRENT FILING DATE: 1998-06-23
; EARLIER APPLICATION NUMBER: 07/869,933
; EARLIER FILING DATE: 1992-04-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-103-663-11

Query Match 100.0%; Score 1390; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 6.1e-127;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db           1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy          61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
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Db          61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy         121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
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Qy         181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
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Qy         241 KGFRLLNPHPKPNPKNN 257
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Db         241 KGFRLLNPHPKPNPKNN 257
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RESULT 4
US-09-285-873-2
; Sequence 2, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation

```
;       STREET:  1825 Sharp Point Drive
;       CITY:  Fort Collins
;       STATE:  Colorado
;       COUNTRY:  USA
;       ZIP:  80525
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  Windows 95
;       SOFTWARE:  WordPerfect for Windows, Version 7.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/285,873
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/756,387
;       FILING DATE:  No. 6309832ember 26, 1996
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Verser, Carol Talkington
;       REGISTRATION NUMBER:  37,459
;       REFERENCE/DOCKET NUMBER:  DI-1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  970/493-7272
;       TELEFAX:  970/484-9505
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  257 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-09-285-873-2

  Query Match             100.0%;  Score 1390;  DB 4;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-127;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
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Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
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Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
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Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
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Db        241 KGFRLLNPHPKPNPKNN 257


RESULT 5
US-08-897-956A-1
; Sequence 1, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
;  APPLICANT:  Mary Ellen Digan
;  APPLICANT:  Philip Lake
;  APPLICANT:  Hermann Gram
;  TITLE OF INVENTION:  Fusion Polypeptides
;  FILE REFERENCE:  600-7244/CPA
;  CURRENT APPLICATION NUMBER: US/08/897,956A
;  CURRENT FILING DATE:  1997-07-21
;  PRIOR APPLICATION NUMBER:  60/022,689
;  PRIOR FILING DATE:  1996-07-26
;  NUMBER OF SEQ ID NOS:  38
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 257
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-08-897-956A-1

  Query Match             100.0%;  Score 1390;  DB 4;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-127;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
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Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||||||||||
Db        241 KGFRLLNPHPKPNPKNN 257


RESULT 6
US-09-944-277A-2
; Sequence 2, Application US/09944277A
; Patent No. 6682894
;   GENERAL INFORMATION:
;       APPLICANT: Frank, Glenn R.
;                  Porter, James P.
;                  Rushlow, Keith E.
;                  Wassom, Donald L.
;       TITLE OF INVENTION: Method to Detect IgE
;       NUMBER OF SEQUENCES: 13
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Carol Talkington Verser, Ph.D.
;                       Heska Corporation
;            STREET: 1825 Sharp Point Drive
;            CITY: Fort Collins
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80525
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: Windows 95
;            SOFTWARE: WordPerfect for Windows, Version 7.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/944,277A
;            FILING DATE: 30-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/285,873
;            FILING DATE: 1999-03-31
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Verser, Carol Talkington
;            REGISTRATION NUMBER: 37,459
;            REFERENCE/DOCKET NUMBER: DI-1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 970/493-7272
;            TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 257 amino acids
;            TYPE: amino acid
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;            TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-944-277A-2

  Query Match            100.0%;  Score 1390;  DB 4;  Length 257;
  Best Local Similarity  100.0%;  Pred. No. 6.1e-127;
  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||||||||||
Db        241 KGFRLLNPHPKPNPKNN 257


RESULT 7
US-07-869-933-13
; Sequence 13, Application US/07869933
; Patent No. 5770396
;  GENERAL INFORMATION:
;    APPLICANT:  KINET, Jean-Pierre
;    TITLE OF INVENTION:  ISOLATION, CHARACTERIZATION, AND USE OF
;    TITLE OF INVENTION:  THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
;    TITLE OF INVENTION:  IMMUNOGLOBULIN
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/869,933
;      FILING DATE:  19920416
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  40399/154 NIHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  232 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  homo sapien
;      STRAIN:  FcRI alpha subunit
US-07-869-933-13

  Query Match            90.9%;  Score 1264;  DB 1;  Length 232;
  Best Local Similarity  100.0%;  Pred. No. 8.9e-115;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60

Qy         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120

Qy        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180

Qy        206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232


RESULT 8
US-08-756-387B-6
; Sequence 6, Application US/08756387B
; Patent No. 5945294
;  GENERAL INFORMATION:
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Porter, James P.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wassom, Donald L.
;    TITLE OF INVENTION:  Method to Detect IgE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carol Talkington Verser, Ph.D.
;      ADDRESSEE:  Heska Corporation
;      STREET:  1825 Sharp Point Drive
;      CITY:  Fort Collins
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80525
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect for Windows, Version 7.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/756,387B
;      FILING DATE:  No. 5945294ember 26, 1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Verser, Carol Talkington
;      REGISTRATION NUMBER:  37,459
;      REFERENCE/DOCKET NUMBER:  DI-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  970/493-7272
;      TELEFAX:  970/484-9505
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  232 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-756-387B-6

  Query Match            90.9%;  Score 1264;  DB 2;  Length 232;
  Best Local Similarity  100.0%;  Pred. No. 8.9e-115;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
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Qy          86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120

Qy         146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180

Qy         206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232


RESULT 9
US-09-103-663-13
; Sequence 13, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
;  APPLICANT: Kinet et al.
;  TITLE OF INVENTION: Isolation, characterization, and use of the human beta
;  TITLE OF INVENTION: subunit of the high affinity receptor for
;  TITLE OF INVENTION: immunoglobulin E.
;  FILE REFERENCE: 50490
;  CURRENT APPLICATION NUMBER: US/09/103,663D
;  CURRENT FILING DATE: 1998-06-23
;  EARLIER APPLICATION NUMBER: 07/869,933
;  EARLIER FILING DATE: 1992-04-16
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 232
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-103-663-13

  Query Match             90.9%;  Score 1264;  DB 3;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-115;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60

Qy          86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120

Qy         146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180

Qy         206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232


RESULT 10
US-09-285-873-6
; Sequence 6, Application US/09285873
; Patent No. 6309832
;  GENERAL INFORMATION:
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Porter, James P.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wassom, Donald L.
;    TITLE OF INVENTION:  Method to Detect IgE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carol Talkington Verser, Ph.D.
;      ADDRESSEE:  Heska Corporation
;      STREET:  1825 Sharp Point Drive
;      CITY:  Fort Collins
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80525
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect for Windows, Version 7.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/285,873
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/756,387
;      FILING DATE:  No. 6309832ember 26, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Verser, Carol Talkington
;      REGISTRATION NUMBER:  37,459
;      REFERENCE/DOCKET NUMBER:  DI-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  970/493-7272
;      TELEFAX:  970/484-9505
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  232 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-285-873-6

  Query Match             90.9%;  Score 1264;  DB 4;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-115;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60

Qy          86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120

Qy         146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180

Qy         206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232


RESULT 11
US-09-944-277A-6
; Sequence 6, Application US/09944277A
; Patent No. 6682894
;  GENERAL INFORMATION:
;       APPLICANT: Frank, Glenn R.
;                  Porter, James P.
;                  Rushlow, Keith E.
;                  Wassom, Donald L.
;       TITLE OF INVENTION: Method to Detect IgE
;       NUMBER OF SEQUENCES: 13
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Carol Talkington Verser, Ph.D.
;                       Heska Corporation
;            STREET: 1825 Sharp Point Drive
;            CITY: Fort Collins
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80525
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
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;              OPERATING SYSTEM: Windows 95
;              SOFTWARE: WordPerfect for Windows, Version 7.0
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/944,277A
;              FILING DATE: 30-Aug-2001
;              CLASSIFICATION: <Unknown>
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 09/285,873
;              FILING DATE: 1999-03-31
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Verser, Carol Talkington
;              REGISTRATION NUMBER: 37,459
;              REFERENCE/DOCKET NUMBER: DI-1
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 970/493-7272
;              TELEFAX: 970/484-9505
;    INFORMATION FOR SEQ ID NO: 6:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 232 amino acids
;              TYPE: amino acid
;              TOPOLOGY: linear
;         MOLECULE TYPE: protein
;         SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-944-277A-6

  Query Match             90.9%;  Score 1264;  DB 4;  Length 232;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-115;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60

Qy         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120

Qy        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180

Qy        206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232


RESULT 12
US-08-897-956A-3
; Sequence 3, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
;  APPLICANT:  Mary Ellen Digan
;  APPLICANT:  Philip Lake
;  APPLICANT:  Hermann Gram
;  TITLE OF INVENTION:  Fusion Polypeptides
;  FILE REFERENCE:  600-7244/CPA
;  CURRENT APPLICATION NUMBER: US/08/897,956A
;  CURRENT FILING DATE:  1997-07-21
;  PRIOR APPLICATION NUMBER:  60/022,689
;  PRIOR FILING DATE:  1996-07-26
;  NUMBER OF SEQ ID NOS:  38
;  SOFTWARE:  FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 978
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion polypeptide
US-08-897-956A-3

  Query Match             80.4%;  Score 1117;  DB 4;  Length 978;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-99;
  Matches  204;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKAPREKYWL 204
              ||||||||||||||||||||||||
Db        181 WQLDYESEPLNITVIKAPREKYWL 204


RESULT 13
US-08-756-387B-11
; Sequence 11, Application US/08756387B
; Patent No. 5945294
;  GENERAL INFORMATION:
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Porter, James P.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wassom, Donald L.
;    TITLE OF INVENTION:  Method to Detect IgE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carol Talkington Verser, Ph.D.
;      ADDRESSEE:  Heska Corporation
;      STREET:  1825 Sharp Point Drive
;      CITY:  Fort Collins
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80525
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect for Windows, Version 7.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/756,387B
;      FILING DATE:  No. 5945294ember 26, 1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Verser, Carol Talkington
;      REGISTRATION NUMBER:  37,459
;      REFERENCE/DOCKET NUMBER:  DI-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  970/493-7272
;      TELEFAX:  970/484-9505
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  197 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-756-387B-11

  Query Match             77.2%;  Score 1073;  DB 2;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-96;
  Matches  197;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
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Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKA 197
              |||||||||||||||||
Db        181 WQLDYESEPLNITVIKA 197


RESULT 14
US-09-285-873-11
; Sequence 11, Application US/09285873
; Patent No. 6309832
;  GENERAL INFORMATION:
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Porter, James P.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wassom, Donald L.
;    TITLE OF INVENTION:  Method to Detect IgE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carol Talkington Verser, Ph.D.
;      ADDRESSEE:  Heska Corporation
;      STREET:  1825 Sharp Point Drive
;      CITY:  Fort Collins
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80525
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect for Windows, Version 7.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/285,873
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/756,387
;      FILING DATE:  No. 6309832ember 26, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Verser, Carol Talkington
;      REGISTRATION NUMBER:  37,459
;      REFERENCE/DOCKET NUMBER:  DI-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  970/493-7272
;      TELEFAX:  970/484-9505
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  197 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-285-873-11

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US-09-944-277A-11
; Sequence 11, Application US/09944277A
; Patent No. 6682894
;  GENERAL INFORMATION:
;       APPLICANT: Frank, Glenn R.
;                  Porter, James P.
;                  Rushlow, Keith E.
;                  Wassom, Donald L.
;       TITLE OF INVENTION: Method to Detect IgE
;       NUMBER OF SEQUENCES: 13
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Carol Talkington Verser, Ph.D.
;                       Heska Corporation
;            STREET: 1825 Sharp Point Drive
;            CITY: Fort Collins
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80525
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: Windows 95
;            SOFTWARE: WordPerfect for Windows, Version 7.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/944,277A
;            FILING DATE: 30-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/285,873
;            FILING DATE: 1999-03-31
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Verser, Carol Talkington
;            REGISTRATION NUMBER: 37,459
;            REFERENCE/DOCKET NUMBER: DI-1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 970/493-7272
;            TELEFAX: 970/484-9505
;  INFORMATION FOR SEQ ID NO: 11:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 197 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-944-277A-11

  Query Match             77.2%;  Score 1073;  DB 4;  Length 197;
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 6, 2004, 09:03:44 ; Search time 78.4779 Seconds
(without alignments)
1053.831 Million cell updates/sec

Title: US-10-763-400-2
Perfect score: 1390
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1390	100.0	257	9	US-09-944-277A-2	Sequence 2, Appli
2	1390	100.0	257	12	US-10-236-392-28	Sequence 28, Appl
3	1390	100.0	257	14	US-10-384-850-45	Sequence 45, Appl
4	1264	90.9	232	9	US-09-944-277A-6	Sequence 6, Appli
5	1157.5	83.3	218	12	US-10-236-392-30	Sequence 30, Appl
6	1073	77.2	197	9	US-09-944-277A-11	Sequence 11, Appl
7	969	69.7	176	10	US-09-809-715-2	Sequence 2, Appli
8	969	69.7	176	12	US-10-293-992-2	Sequence 2, Appli
9	947	68.1	172	9	US-09-944-277A-13	Sequence 13, Appl
10	947	68.1	172	9	US-09-245-764-9	Sequence 9, Appli
11	947	68.1	172	12	US-10-293-992-4	Sequence 4, Appli
12	947	68.1	172	12	US-10-687-109-9	Sequence 9, Appli
13	944	67.9	176	10	US-09-809-715-4	Sequence 4, Appli
14	832.5	59.9	255	15	US-10-434-817-2	Sequence 2, Appli
15	799.5	57.5	236	15	US-10-434-817-7	Sequence 7, Appli
16	617	44.4	201	15	US-10-434-817-12	Sequence 12, Appl
17	423	30.4	254	15	US-10-449-566-117	Sequence 117, App
18	419	30.1	254	14	US-10-027-736A-20	Sequence 20, Appl
19	418	30.1	254	14	US-10-384-850-44	Sequence 44, Appl
20	418	30.1	254	14	US-10-027-736A-21	Sequence 21, Appl
21	418	30.1	254	15	US-10-449-566-116	Sequence 116, App
22	411	29.6	233	15	US-10-193-377-6	Sequence 6, Appli
23	409.5	29.5	234	14	US-10-027-736A-69	Sequence 69, Appl
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25	380.5	27.4	294	14	US-10-027-736A-18	Sequence 18, Appl
26	379	27.3	374	12	US-09-836-544-23	Sequence 23, Appl
27	379	27.3	374	14	US-10-027-736A-10	Sequence 10, Appl
28	379	27.3	404	15	US-10-193-377-7	Sequence 7, Appli
29	376	27.1	374	14	US-10-308-279-30	Sequence 30, Appl
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31	374.5	26.9	336	14	US-10-027-736A-65	Sequence 65, Appl
32	374	26.9	291	14	US-10-027-736A-19	Sequence 19, Appl
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34	372	26.8	399	9	US-09-925-301-1128	Sequence 1128, Ap
35	372	26.8	399	14	US-10-106-698-5782	Sequence 5782, Ap
36	371.5	26.7	310	14	US-10-384-850-42	Sequence 42, Appl
37	371.5	26.7	310	16	US-10-322-696-180	Sequence 180, App
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40	366	26.3	298	16	US-10-322-696-93	Sequence 93, Appl
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43	357	25.7	174	12	US-10-687-109-8	Sequence 8, Appli
44	357	25.7	261	9	US-09-245-764-7	Sequence 7, Appli
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ALIGNMENTS

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RESULT 1
US-09-944-277A-2
; Sequence 2, Application US/09944277A
; Patent No. US20020034771A1
;  GENERAL INFORMATION:
;       APPLICANT: Frank, Glenn R.
;                  Porter, James P.
;                  Rushlow, Keith E.
;                  Wassom, Donald L.
;       TITLE OF INVENTION: Method to Detect IgE
;       NUMBER OF SEQUENCES: 13
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Carol Talkington Verser, Ph.D.
;                       Heska Corporation
;            STREET: 1825 Sharp Point Drive
;            CITY: Fort Collins
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80525
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: Windows 95
;            SOFTWARE: WordPerfect for Windows, Version 7.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/944,277A
;            FILING DATE: 30-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/285,873
;            FILING DATE: 1999-03-31
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Verser, Carol Talkington
;            REGISTRATION NUMBER: 37,459
;            REFERENCE/DOCKET NUMBER: DI-1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 970/493-7272
;            TELEFAX: 970/484-9505
;
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;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 257 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-944-277A-2

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  Matches  257;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
US-10-236-392-28
; Sequence 28, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, David W
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Burgess, Catherine, E
;  APPLICANT:  Casman, Stacie J
;  APPLICANT:  Catterton, Elina
;  APPLICANT:  Chapoval, Andrei
;  APPLICANT:  Crabtree, Julie
;  APPLICANT:  Edinger, Shlomit, R
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Gusev, Vladamir
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  LaRochelle, William J
;  APPLICANT:  Li, Li
;  APPLICANT:  MacDougall, John R
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Miller, Charles E
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Pena, Carol A
;  APPLICANT:  Peyman, John A
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Reiger, Daniel K
;  APPLICANT:  Rothenberg, Mark E
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-442A
;  CURRENT APPLICATION NUMBER: US/10/236,392
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US09/540,763
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: US60/390,155
;  PRIOR FILING DATE: 2002-06-19
;  PRIOR APPLICATION NUMBER: US09/635,949
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: US60/318,765
;  PRIOR FILING DATE: 2001-09-12
;  PRIOR APPLICATION NUMBER: US60/357,303
;  PRIOR FILING DATE: 2002-02-15
;  PRIOR APPLICATION NUMBER: US60/367,753
;  PRIOR FILING DATE: 2002-03-25
;  PRIOR APPLICATION NUMBER: US60/369,479
;  PRIOR FILING DATE: 2002-04-02
;  PRIOR APPLICATION NUMBER: US09/659,634
;  PRIOR FILING DATE: 2000-09-12
;  PRIOR APPLICATION NUMBER: US60/318,120
;  PRIOR FILING DATE: 2001-09-07
;  PRIOR APPLICATION NUMBER: US60/318,130
;  PRIOR FILING DATE: 2001-09-07
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 794
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; SEQ ID NO 28
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;   TYPE: PRT
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US-10-236-392-28

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Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
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RESULT 3
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; Publication No. US20030175890A1
; GENERAL INFORMATION:
;  APPLICANT: C. Fraser
;  TITLE OF INVENTION: FAIL MOLECULES AND USES THEREOF
;  FILE REFERENCE: 7853-217
;  CURRENT APPLICATION NUMBER: US/10/384,850
;  CURRENT FILING DATE:  2003-03-10
;  PRIOR APPLICATION NUMBER: US/09/702,021
;  PRIOR FILING DATE: 2000-10-30
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: FastSEQ for Windows Version 3.0
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US-10-384-850-45
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Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
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RESULT 4
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; Sequence 6, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 232 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-944-277A-6

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  Query Match           90.9%;  Score 1264;  DB 9;  Length 232;
  Best Local Similarity  100.0%;  Pred. No. 1.9e-100;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60

Qy         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120

Qy        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180

Qy        206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
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RESULT 5
US-10-236-392-30
; Sequence 30, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladamir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRochelle, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479

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;  PRIOR FILING DATE: 2002-04-02
;  PRIOR APPLICATION NUMBER: US09/659,634
;  PRIOR FILING DATE: 2000-09-12
;  PRIOR APPLICATION NUMBER: US60/318,120
;  PRIOR FILING DATE: 2001-09-07
;  PRIOR APPLICATION NUMBER: US60/318,130
;  PRIOR FILING DATE: 2001-09-07
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 794
;  SOFTWARE: Custom
; SEQ ID NO 30
;   LENGTH: 218
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-236-392-30

  Query Match             83.3%;  Score 1157.5;  DB 12;  Length 218;
  Best Local Similarity   84.8%;  Pred. No. 2.5e-91;
  Matches  218;  Conservative    0;  Mismatches    0;  Indels   39;  Gaps    1;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYK---------------------------- 92

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
                          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         93 -----------CHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 141

Qy        181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        142 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 201

Qy        241 KGFRLLNPHPKPNPKNN 257
              |||||||||||||||||
Db        202 KGFRLLNPHPKPNPKNN 218


RESULT 6
US-09-944-277A-11
; Sequence 11, Application US/09944277A
; Patent No. US20020034771A1
;   GENERAL INFORMATION:
;        APPLICANT: Frank, Glenn R.
;                   Porter, James P.
;                   Rushlow, Keith E.
;                   Wassom, Donald L.
;        TITLE OF INVENTION: Method to Detect IgE
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Carol Talkington Verser, Ph.D.
;                        Heska Corporation
;             STREET: 1825 Sharp Point Drive
;             CITY: Fort Collins
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80525
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: WordPerfect for Windows, Version 7.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/944,277A
;             FILING DATE: 30-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/285,873
;             FILING DATE: 1999-03-31
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Verser, Carol Talkington
;             REGISTRATION NUMBER: 37,459
;             REFERENCE/DOCKET NUMBER: DI-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 970/493-7272
;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 197 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-944-277A-11

  Query Match             77.2%;  Score 1073;  DB 9;  Length 197;
  Best Local Similarity   100.0%;  Pred. No. 4e-84;
  Matches  197;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy        181 WQLDYESEPLNITVIKA 197
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Db        181 WQLDYESEPLNITVIKA 197


RESULT 7
US-09-809-715-2
; Sequence 2, Application US/09809715
; Publication No. US20030003502A1
; GENERAL INFORMATION:
;  APPLICANT: Jardetzky, Theodore S.
;  APPLICANT:  Garman, Scott Clayton
;  APPLICANT:  Wurzburg, Beth A.
;  APPLICANT:  Kinet, Jean-Pierre
;  TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A Fc
;  TITLE OF INVENTION:  EPSILON RECEPTOR ALPHA CHAIN AND A Fc REGION OF AN IgE
;  TITLE OF INVENTION:  ANTIBODY AND USES THEREOF
;  FILE REFERENCE: AL-8
;  CURRENT APPLICATION NUMBER: US/09/809,715
;  CURRENT FILING DATE:  2001-03-14
;  PRIOR APPLICATION NUMBER: 60/189,853
;  PRIOR FILING DATE: 2000-03-15
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 176
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-809-715-2

  Query Match             69.7%;  Score 969;  DB 10;  Length 176;
  Best Local Similarity   100.0%;  Pred. No. 3e-75;
  Matches  176;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60

Qy         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120
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Qy        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREK 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREK 176


RESULT 8
US-10-293-992-2
; Sequence 2, Application US/10293992
; Publication No. US20040033527A1
; GENERAL INFORMATION:
;  APPLICANT: Jardetzky, Theodore S.
;  APPLICANT:  Garman, Scott Clayton
;  APPLICANT:  Kinet, Jean-Pierre
;  TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A Fc EPSILON RECEPT
;  TITLE OF INVENTION:  CHAIN
;  FILE REFERENCE: AL-3-C1-1
;  CURRENT APPLICATION NUMBER: US/10/293,992
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: 09/434,193
;  PRIOR FILING DATE: 1999-11-04
;  PRIOR APPLICATION NUMBER: 60/107,219
;  PRIOR FILING DATE: 1998-11-05
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 176
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-992-2

  Query Match             69.7%;  Score 969;  DB 12;  Length 176;
  Best Local Similarity   100.0%;  Pred. No. 3e-75;
  Matches  176;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60

Qy         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120

Qy        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREK 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREK 176


RESULT 9
US-09-944-277A-13
; Sequence 13, Application US/09944277A
; Patent No. US20020034771A1
;   GENERAL INFORMATION:
;        APPLICANT: Frank, Glenn R.
;                   Porter, James P.
;                   Rushlow, Keith E.
;                   Wassom, Donald L.
;        TITLE OF INVENTION: Method to Detect IgE
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Carol Talkington Verser, Ph.D.
;                        Heska Corporation
;             STREET: 1825 Sharp Point Drive
;             CITY: Fort Collins
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80525
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: WordPerfect for Windows, Version 7.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/944,277A
;             FILING DATE: 30-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/285,873
;             FILING DATE: 1999-03-31
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Verser, Carol Talkington
;             REGISTRATION NUMBER: 37,459
;             REFERENCE/DOCKET NUMBER: DI-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 970/493-7272
;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 13:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 172 amino acids
;             TYPE: amino acid
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-944-277A-13

  Query Match             68.1%;  Score 947;  DB 9;  Length 172;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-73;
  Matches  172;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60

Qy         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120

Qy        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKA 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKA 172


RESULT 10
US-09-245-764-9
; Sequence 9, Application US/09245764
; Patent No. US20020107359A1
; GENERAL INFORMATION:
;  APPLICANT: Hogarth, P. Mark
;  APPLICANT: Powell, Maree S.
;  APPLICANT: McKenzie, Ian F.C.
;  APPLICANT: Maxwell, Kelly F.
;  APPLICANT: Garrett, Thomas P.J.
;  APPLICANT: Epa, Vidana
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF Fc RECEPTORS
;  TITLE OF INVENTION: AND USES THEREOF
;  FILE REFERENCE: 4102-4
;  CURRENT APPLICATION NUMBER: US/09/245,764
;  CURRENT FILING DATE: 1999-02-05
;  EARLIER APPLICATION NUMBER: 60/099,994
;  EARLIER FILING DATE: 1998-09-11
;  EARLIER APPLICATION NUMBER: 60/073,972
;  EARLIER FILING DATE: 1998-02-06
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 172
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-245-764-9

  Query Match             68.1%;  Score 947;  DB 9;  Length 172;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-73;
  Matches  172;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
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Qy          86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120

Qy         146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKA 197
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKA 172


RESULT 11
US-10-293-992-4
; Sequence 4, Application US/10293992
; Publication No. US20040033527A1
; GENERAL INFORMATION:
;  APPLICANT: Jardetzky, Theodore S.
;  APPLICANT:  Garman, Scott Clayton
;  APPLICANT:  Kinet, Jean-Pierre
;  TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A Fc EPSILON RECEPT
;  TITLE OF INVENTION:  CHAIN
;  FILE REFERENCE: AL-3-C1-1
;  CURRENT APPLICATION NUMBER: US/10/293,992
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: 09/434,193
;  PRIOR FILING DATE: 1999-11-04
;  PRIOR APPLICATION NUMBER: 60/107,219
;  PRIOR FILING DATE: 1998-11-05
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
;   LENGTH: 172
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-293-992-4

  Query Match             68.1%;  Score 947;  DB 12;  Length 172;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-73;
  Matches  172;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60

Qy          86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120

Qy         146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKA 197
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKA 172


RESULT 12
US-10-687-109-9
; Sequence 9, Application US/10687109
; Publication No. US20040054480A1
; GENERAL INFORMATION:
;  APPLICANT: Hogarth, P. Mark
;  APPLICANT:  Powell, Maree S.
;  APPLICANT:  McKenzie, Ian F.C.
;  APPLICANT:  Maxwell, Kelly F.
;  APPLICANT:  Garrett, Thomas P.J.
;  APPLICANT:  Epa, Vidana
;  TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES AND MODELS OF Fc RECEPTORS
;  TITLE OF INVENTION:  AND USES THEREOF
;  FILE REFERENCE: 4102-4
;  CURRENT APPLICATION NUMBER: US/10/687,109
;  CURRENT FILING DATE:  2003-10-15
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/245,764
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-05
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/099,994
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-09-11
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/073,972
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-06
;  NUMBER OF SEQ ID NOS: 15
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
;   LENGTH: 172
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-687-109-9

  Query Match             68.1%;  Score 947;  DB 12;  Length 172;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-73;
  Matches  172;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60

Qy          86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120

Qy         146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKA 197
               |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKA 172


RESULT 13
US-09-809-715-4
; Sequence 4, Application US/09809715
; Publication No. US20030003502A1
; GENERAL INFORMATION:
;  APPLICANT: Jardetzky, Theodore S.
;  APPLICANT:  Garman, Scott Clayton
;  APPLICANT:  Wurzburg, Beth A.
;  APPLICANT:  Kinet, Jean-Pierre
;  TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A Fc
;  TITLE OF INVENTION:  EPSILON RECEPTOR ALPHA CHAIN AND A Fc REGION OF AN IgE
;  TITLE OF INVENTION:  ANTIBODY AND USES THEREOF
;  FILE REFERENCE: AL-8
;  CURRENT APPLICATION NUMBER: US/09/809,715
;  CURRENT FILING DATE:  2001-03-14
;  PRIOR APPLICATION NUMBER: 60/189,853
;  PRIOR FILING DATE: 2000-03-15
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 176
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-809-715-4

  Query Match             67.9%;  Score 944;  DB 10;  Length 176;
  Best Local Similarity   97.7%;  Pred. No. 4.2e-73;
  Matches  172;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60

Qy          86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145
               |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 EDSGEYKCQHQQVAESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120

Qy         146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREK 201
               |||||||||||||| ||||||  |||||||||||||||||||||||||||||||||
Db         121 YKDGEALKYWYENHAISITNAAAEDSGTYYCTGKVWQLDYESEPLNITVIKAPREK 176


RESULT 14
US-10-434-817-2
; Sequence 2, Application US/10434817
; Publication No. US20030235579A1
;   GENERAL INFORMATION:
```

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;       APPLICANT: Weber, Eric R.
;                  McCall, Catherine A.
;       TITLE OF INVENTION: NOVEL EQUINE Fc EPSILON RECEPTOR ALPHA
;                           CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
;       NUMBER OF SEQUENCES: 12
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Heska Corporation
;            STREET: 1825 Sharp Point Drive
;            CITY: Fort Collins
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80525
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WordPerfect for Windows, Version 7.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/434,817
;            FILING DATE: 08-May-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/015,734
;            FILING DATE: 29-JAN-1998
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Verser, Carol Talkington
;            REGISTRATION NUMBER: 37,459
;            REFERENCE/DOCKET NUMBER: DI-4
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 970/493-7272
;            TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 255 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: Protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-434-817-2

  Query Match           59.9%;  Score 832.5;  DB 15;  Length 255;
  Best Local Similarity  63.9%;  Pred. No. 2.5e-63;
  Matches  163;  Conservative   31;  Mismatches   56;  Indels    5;  Gaps    2;

Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
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Db          1 MPAPMGSPALLWITFLLFSLDGVPAAIRKSTVSLNPPWNRIFRGENVTLTCNKNKPLKGN 60

Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||:| :| :  | | ||||| ||    ||||:|::  :| || |:|||||||||||||||
Db         61 STEWTYNNTTLEVTTSSLNITNASHRSSGEYRCRNNDLNLSEAVHLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTG-- 178
               |:||: | ||| ||::|||:|||||||: |:||||| |||| :|| |:|||||| |
Db        121 EVIEGKALVLRCRGWKDWDVFKVIYYKDGKPLEYWYENKNISIESATTENSGTYYCEGAF 180

Qy        179 --KVWQLDYESEPLNITVIKAPREK-YWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLK 235
                 |      | |: ||||| || : | ||||| |||||||||||||||:|||||:|||||
Db        181 NFKRTSERYTSDYLNITVKKAEQSKRYWLQFIIPLLVVILFAVDTGLFVSTQQQLTFLLK 240

Qy        236 IKRTRKGFRLLNPHP 250
              |||||:| :|::|||
Db        241 IKRTRRGRKLMDPHP 255


RESULT 15
US-10-434-817-7
; Sequence 7, Application US/10434817
; Publication No. US20030235579A1
;   GENERAL INFORMATION:
;       APPLICANT: Weber, Eric R.
;                  McCall, Catherine A.
;       TITLE OF INVENTION: NOVEL EQUINE Fc EPSILON RECEPTOR ALPHA
;                           CHAIN NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
;       NUMBER OF SEQUENCES: 12
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Heska Corporation
;            STREET: 1825 Sharp Point Drive
;            CITY: Fort Collins
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80525
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WordPerfect for Windows, Version 7.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/434,817
;            FILING DATE: 08-May-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/015,734
;            FILING DATE: 29-JAN-1998
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Verser, Carol Talkington
;            REGISTRATION NUMBER: 37,459
;            REFERENCE/DOCKET NUMBER: DI-4
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 970/493-7272
;            TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 236 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: Protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-434-817-7

  Query Match           57.5%;  Score 799.5;  DB 15;  Length 236;
  Best Local Similarity  66.0%;  Pred. No. 1.5e-60;
  Matches  155;  Conservative   29;  Mismatches   46;  Indels    5;  Gaps    2;

Qy         21 DGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNI 80
              ||| |  :|  |||||||||||:||||||||  |   : :||:| :| :  | | |||||
Db          2 DGVPAAIRKSTVSLNPPWNRIFRGENVTLTCNKNKPLKGNSTEWTYNNTTLEVTTSSLNI 61

Qy         81 VNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDV 140
               ||     ||||:|::  :| || |:|||||||||||||| |:||: | ||| ||::|||
Db         62 TNASHRSSGEYRCRNNDLNLSEAVHLEVFSDWLLLQASAEEVIEGKALVLRCRGWKDWDV 121

Qy        141 YKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTG----KVWQLDYESEPLNITVIK 196
              :|||||||: |:||||| |||| :|| |:|||||| |     |     | |: |||||| |
Db        122 FKVIYYKDGKPLEYWYENKNISIESATTENSGTYYCEGAFNFKRTSERYTSDYLNITVKK 181

Qy        197 APREK-YWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHP 250
              | : | ||||| |||||||||||||||:|||||:||||||||||:| :|::|||
Db        182 AEQSKRYWLQFIIPLLVVILFAVDTGLFVSTQQQLTFLLKIKRTRRGRKLMDPHP 236


Search completed: October  6, 2004, 09:28:09
Job time : 80.4779 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 6, 2004, 09:03:14 ; Search time 14.0781 Seconds
(without alignments)
1756.007 Million cell updates/sec

Title: US-10-763-400-2
Perfect score: 1390
Sequence: 1 MAPAMESPTLLCVALLFFAP.....RTRKGFRLLNPHPKPNPKNN 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1390	100.0	257	2	S00682	IgE Fc receptor al
2	626.5	45.1	250	2	A34342	IgE Fc receptor al
3	597.5	43.0	245	2	A30154	IgE receptor alpha
4	418	30.1	254	1	JL0107	Fc gamma (IgG) rec
5	406	29.2	233	1	JU0284	Fc gamma (IgG) rec
6	405	29.1	296	2	I46021	Fc-gamma receptor
7	403	29.0	280	2	I55577	Fc gamma (IgG) rec
8	401.5	28.9	261	2	S29360	Fc gamma (IgG) rec
9	399	28.7	267	2	I56110	Fc-gamma RIIIB-alp
10	395	28.4	267	2	A35902	Fc gamma (IgG) rec
11	390.5	28.1	270	2	A34636	Fc-gamma receptor
12	380	27.3	267	2	I72882	Fc gamma receptor
13	379	27.3	336	2	I48471	Fc gamma (IgG) rec
14	379	27.3	404	2	A46480	Fc gamma (IgG) rec
15	376	27.1	344	2	A41357	Fc gamma (IgG) rec
16	376	27.1	374	1	A39878	Fc gamma (IgG) rec
17	371.5	26.7	323	2	S06946	Fc gamma (IgG) rec
18	368	26.5	285	2	S36903	Fc gamma (IgG) rec
19	367.5	26.4	310	2	JL0119	Fc gamma (IgG) rec
20	367	26.4	283	1	FCMSG1	Fc gamma (IgG) rec
21	367	26.4	330	2	A40071	Fc gamma (IgG) rec
22	367	26.4	330	2	I49660	Fc-gamma-1/gamma-2
23	348	25.0	157	2	D31327	IgE receptor alpha
24	347	25.0	317	2	JL0118	Fc gamma (IgG) rec
25	338	24.3	160	2	I47163	cytolytic trigger
26	271	19.5	159	2	I47164	cytolytic trigger
27	166	11.9	1694	2	S50065	sialoadhesin - mou
28	156	11.2	104	2	I47165	cytolytic trigger
29	137.5	9.9	458	1	WMMSR1	biliary glycoprote
30	137.5	9.9	521	2	JC1508	biliary glycoprote
31	136.5	9.8	458	2	JC1509	biliary glycoprote
32	136.5	9.8	458	2	S23969	cell-adhesion mole
33	136.5	9.8	458	2	S68177	C-CAM2a protein is
34	136.5	9.8	519	2	A44783	ecto-ATPase precur
35	136.5	9.8	521	2	S34338	biliary glycoprote
36	134	9.6	7962	2	I38346	elastic titin - hu
37	133	9.6	538	2	JC2457	vascular cell adhe
38	129.5	9.3	344	2	A27681	nonspecific cross-
39	129.5	9.3	1239	1	A32579	neuroglian - fruit
40	126	9.1	1327	2	T09402	immunoglobulin-lik
41	125.5	9.0	978	2	S16385	macrophage colony-
42	124.5	9.0	1033	2	S19247	cell adhesion prot
43	123.5	8.9	264	2	I46020	FC gamma 2 recepto
44	123.5	8.9	976	1	TVMSMD	macrophage colony-
45	121.5	8.7	739	2	JS0675	vascular cell adhe

ALIGNMENTS

RESULT 1
S00682
IgE Fc receptor alpha chain precursor - human
N;Alternate names: Fc-epsilon receptor
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 23-Jul-1999
C;Accession: S00682; B30154; S42209
R;Kochan, J.; Pettine, L.F.; Hakimi, J.; Kishi, K.; Kinet, J.P.
Nucleic Acids Res. 16, 3584, 1988
A;Title: Isolation of the gene coding for the alpha subunit of the human high affinity I
A;Reference number: S00682; MUID:88233953; PMID:2967464
A;Accession: S00682
A;Molecule type: mRNA
A;Residues: 1-257 <KOC>
A;Cross-references: EMBL:X06948; NID:g31317; PIDN:CAA30025.1; PID:g31318
R;Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.
Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988
A;Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterizat
A;Reference number: A94191; MUID:88158102; PMID:2964640
A;Accession: B30154
A;Molecule type: mRNA
A;Residues: 1-257 <SHI>
A;Cross-references: GB:J03605; NID:g187449; PIDN:AAA36204.1; PID:g307164
R;Yagi, S.; Yanagida, M.; Tanida, I.; Hasegawa, A.; Okumura, K.; Ra, C.
Eur. J. Biochem. 220, 593-598, 1994
A;Title: High-level expression of the truncated alpha chain of human high-affinity recep
nant product.
A;Reference number: S42209; MUID:94170811; PMID:8125119
A;Accession: S42209
A;Molecule type: protein
A;Residues: 26-197 <YAG>
A;Experimental source: purified recombinant protein
C;Genetics:
A;Gene: GDB:FCER1A
A;Cross-references: GDB:119902; OMIM:147140
A;Map position: 1q23-1q23
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: immunoglobulin receptor; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-257/Product: IgE Fc receptor alpha chain #status predicted <MAT>
F;44-95/Domain: immunoglobulin homology <IMM1>
F;125-178/Domain: immunoglobulin homology <IMM2>

Query Match 100.0%; Score 1390; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 5.2e-100;
Matches 257; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
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Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
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Db          61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120

Qy         121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKV 180

Qy         181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 WQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTR 240

Qy         241 KGFRLLNPHPKPNPKNN 257
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Db         241 KGFRLLNPHPKPNPKNN 257


RESULT 2
A34342
IgE Fc receptor alpha chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Jun-1990 #sequence_revision 15-Jun-1990 #text_change 23-Jul-1999
C;Accession: A34342; A61238
R;Ra, C.; Jouvin, M.H.E.; Kinet, J.P.
J. Biol. Chem. 264, 15323-15327, 1989
A;Title: Complete structure of the mouse mast cell receptor for IgE (Fc-epsilon-RI) and
A;Reference number: A34342; MUID:89359361; PMID:2527850
A;Accession: A34342
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-250 <RAC>
A;Cross-references: GB:J05018; NID:g193236; PIDN:AAA37600.1; PID:g309224
R;Robertson, M.W.; Mehl, V.S.; Richards, M.L.; Liu, F.T.
Int. Arch. Allergy Appl. Immunol. 96, 289-295, 1991
A;Title: mRNA variants encoding multiple forms of the high-affinity IgE receptor alpha s
A;Reference number: A61238; MUID:92234569; PMID:1839735
A;Accession: A61238
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 125-194 <ROB>
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein
F;42-94/Domain: immunoglobulin homology <IMM>

  Query Match             45.1%;  Score 626.5;  DB 2;  Length 250;
  Best Local Similarity   51.9%;  Pred. No. 3.7e-41;
  Matches  121;  Conservative   46;  Mismatches   63;  Indels    3;  Gaps    3;

Qy          11 LCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEV-SSTKWFHNGS 69
               ||:|||| : | :|   :|  ::|:||| ||| || |||:| |||  :: |:||| |||:
Db           9 LCLALLFMSLDVILTATEKSVLTLDPPWIRIFTGEKVTLSCYGNNHLQMNSTTKWIHNGT 68

Qy          70 LSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLF 129
               :||  :| | ||:|  :|||:| || | : :|:|||| |  |||||| ||:::::
Db          69 VSEVNSSHLVIVSATVQDSGKYICQKQGLFKSKPVYLNVTQDWLLLQTSADMILVHGSFD 128

Qy         130 LRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEP 189
               :|||||:||:| ||||||:  |  | ||:  :||  ||: |||||:| | : |::|||:
Db         129 IRCHGWKNWNVRKVIYYRNDHAFNYSYES-PVSIREATLNDSGTYHCKGYLRQVEYESDK 187

Qy         190 LNITVIKAPREK-YWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRK 241
                 | |:|| : | ||||   |||| |||||||||| :||::|   :|:|::| |
Db         188 FRIAVVKAYKCKYYWLQLIFPLLVAILFAVDTGLLLSTEEQFKSVLEIQKTGK 240


RESULT 3
A30154
IgE receptor alpha chain precursor - rat
N;Alternate names: Fc-epsilon-R alpha chain precursor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 21-Jan-2000
C;Accession: C31327; A31327; A30154; A27116; I55304
R;Liu, F.T.; Albrandt, K.; Robertson, M.W.
Proc. Natl. Acad. Sci. U.S.A. 85, 5639-5643, 1988
A;Title: cDNA heterogeneity suggests structural variants related to the high-affinity Ig
A;Reference number: A94203; MUID:88289772; PMID:2969594
A;Accession: C31327
A;Molecule type: mRNA
A;Residues: 1-245 <LIU>
A;Cross-references: GB:M21622; GB:J03811
A;Experimental source: basophilic leukemia cell line, clone R3-4
A;Accession: A31327
A;Molecule type: mRNA
A;Residues: 21-245 <LI3>
A;Cross-references: GB:M21622; NID:g204109; PIDN:AAA41146.1; PID:g204110; GB:J03811
A;Experimental source: basophilic leukemia cell line
R;Shimizu, A.; Tepler, I.; Benfey, P.N.; Berenstein, E.H.; Siraganian, R.P.; Leder, P.
Proc. Natl. Acad. Sci. U.S.A. 85, 1907-1911, 1988
A;Title: Human and rat mast cell high-affinity immunoglobulin E receptors: characterizat
A;Reference number: A94191; MUID:88158102; PMID:2964640
A;Accession: A30154
A;Molecule type: mRNA
A;Residues: 1-245 <SHI>
A;Cross-references: GB:J03606; NID:g205331; PIDN:AAA41582.1; PID:g205332
R;Kinet, J.P.; Metzger, H.; Hakimi, J.; Kochan, J.
Biochemistry 26, 4605-4610, 1987
A;Title: A cDNA presumptively coding for the alpha subunit of the receptor with high aff
A;Reference number: A27116; MUID:88024987; PMID:2959318
A;Accession: A27116
A;Molecule type: mRNA
A;Residues: 1,'G',3-236,'N',238-244,'RLKPNS' <KIN>
R;Tepler, I.; Shimizu, A.; Leder, P.
J. Biol. Chem. 264, 5912-5915, 1989
A;Title: The gene for the rat mast cell high affinity IgE receptor alpha chain. Structur
A;Reference number: I55304; MUID:89174653; PMID:2522441
A;Accession: I55304
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-16 <RES>
A;Cross-references: GB:M25334; NID:g341335; PIDN:AAA74562.1; PID:g556391
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: immunoglobulin receptor; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-245/Product: IgE receptor alpha chain #status predicted <MAT>
F;42-93/Domain: immunoglobulin homology <IMM>

  Query Match             43.0%;  Score 597.5;  DB 2;  Length 245;
  Best Local Similarity   49.8%;  Pred. No. 6.3e-39;
  Matches  116;  Conservative   43;  Mismatches   73;  Indels    1;  Gaps    1;

Qy          11 LCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSL 70
               ||:||:  :   :|   ||  |||:||| ||  |: ||| ||||  :::|||| || |:
Db           9 LCLALVLISLGVMLTATQKSVVSLDPPWIRILTGDKVTLICNGNNSSQMNSTKWIHNDSI 68

Qy          71 SEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFL 130
               |   :|   ||:|  :|||:| || |   :|:|||| |  :|||||:||:||::    :
Db          69 SNVKSSHWVIVSATIQDSGKYICQKQGFYKSKPVYLNVMQEWLLLQSSADVVLDNGSFDI 128

Qy         131 RCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPL 190
               ||  |: | |:|||||||  | || |:::|||| ||  |||:|:||| : ::: :|:
Db         129 RCRSWKKWKVHKVIYYKDDIAFKYSYDSNNISIRKATFNDSGSYHCTGYLNKVECKSDKF 188

Qy         191 NITVIKAPREKY-WLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKG 242
               :| |:|   :| |||   | | |||||||||: || :|   :|||::| ||
Db         189 SIAVVKDYTIEYRWLQLIFPSLAVILFAVDTGLWFSTHKQFESILKIQKTGKG 241


RESULT 4
JL0107
Fc gamma (IgG) receptor III-A precursor (natural killer cell) [validated] - human
N;Alternate names: CD16 antigen; low affinity IgG Fc receptor type III-2 precursor; surf
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 02-Aug-1996 #text_change 08-Dec-2000
C;Accession: JL0107; A60383; A32933; I37627
R;Ravetch, J.V.; Perussia, B.
J. Exp. Med. 170, 481-497, 1989
A;Title: Alternative membrane forms of Fc gamma RIII(CD16) on human natural killer cells
```

A;Reference number: JL0107; MUID:89328325; PMID:2526846
A;Accession: JL0107
A;Molecule type: mRNA
A;Residues: 1-254 <RAV>
A;Cross-references: GB:X52645; GB:M31937; NID:g31323; PIDN:CAA36870.1; PID:g31324
A;Note: the sequence of the receptor from human polymorphonuclear granulocytes, reported
21 residues
R;Trounstine, M.L.; Peltz, G.A.; Yssel, H.; Huizinga, T.W.J.; von dem Borne, A.E.G.K.; S
Int. Immunol. 2, 303-310, 1990
A;Title: Reactivity of cloned, expressed human FcgammaRIII isoforms with monoclonal anti
A;Reference number: A60383; MUID:91120527; PMID:1703781
A;Accession: A60383
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-254 <TRO>
R;Scallon, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.C
Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989
A;Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phosp
A;Reference number: A32933; MUID:89296947; PMID:2525780
A;Accession: A32933
A;Molecule type: mRNA
A;Residues: 31-254 <SCA>
A;Cross-references: GB:M24853; NID:g184849; PIDN:AAA53506.1; PID:g386806
R;Gessner, J.E.; Grussenmeyer, T.; Kolanus, W.; Schmidt, R.E.
J. Biol. Chem. 270, 1350-1361, 1995
A;Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole
A;Reference number: A55439; MUID:95138131; PMID:7836402
A;Accession: I37627
A;Molecule type: DNA
A;Residues: 1-39 <RES>
A;Cross-references: EMBL:Z46222; NID:g559445; PIDN:CAA86295.1; PID:g1478198
A;Note: translation has been corrected relative to PID:g871305
C;Comment: This low affinity IgG Fc receptor of natural killer cells, which is the produ
e nearly identical, yet this receptor lacks a glycosylphosphatidylinositol anchor and in
C;Genetics:
A;Gene: GDB:FCGR3A; FCGR3
A;Cross-references: GDB:119904; OMIM:146740
A;Map position: 1q23-1q23
A;Introns: 14/1; 21/1
A;Note: the list of introns is incomplete
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: glycoprotein; receptor; transmembrane protein
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-254/Product: Fc gamma (IgG) receptor III-A #status experimental <MAT>
F;18-208/Domain: extracellular #status predicted <EXT>
F;40-91/Domain: immunoglobulin homology <IMM1>
F;111-174/Domain: immunoglobulin homology <IMM2>
F;209-229/Domain: transmembrane #status predicted <TRZ>
F;230-254/Domain: intracellular #status predicted <CYT>
F;56,63,92,180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match 30.1%; Score 418; DB 1; Length 254;
  Best Local Similarity 40.9%; Pred. No. 4.5e-25;
  Matches 94; Conservative 34; Mismatches 92; Indels 10; Gaps 3;

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Qy         10 LLCVALLFFAPDGVLAVPQKPK--VSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHN 67
              ||  |||     | :    ||  | | | | |: : ::||| | |    | :||:||||
Db          5 LLPTALLLLVSAG-MRTEDLPKAVVFLEPQWYRVLEKDSVTLKCQGAYSPEDNSTQWFHN 63

Qy         68 GSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQP 127
              ||      ||  |  |  :||||||:||      |:|| |||   ||||||  |  |  |
Db         64 ESLISSQASSYFIDAATVDDSGEYRCQTNLSTLSDPVQLEVHIGWLLLQAPRWVFKEEDP 123

Qy        128 LFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYES 187
              : |||| |:|  ::|| | ::|:  ||:: | :  |  ||::|||:|:| |     :  |
Db        124 IHLRCHSWKNTALHKVTYLQNGKGRKYFHHNSDFYIPKATLKDSGSYFCRGLFGSKNVSS 183

Qy        188 EPLNITVIKAPREKYWLQFFIP-------LLVVILFAVDTGLFISTQQQV 230
              | :|||: :          || |       |::|:||||||||: | :  :
Db        184 ETVNITITQGLAVSTISSFFPPGYQVSFCLVMVLLFAVDTGLYFSVKTNI 233
```

RESULT 5

JU0284
Fc gamma (IgG) receptor III-B precursor (neutrophil) - human
N;Alternate names: FcR III; IgG Fc receptor precursor, type III-1 (polymorphonuclear gra
C;Species: Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 02-Aug-1996 #text_change 28-Jan-2000
C;Accession: JU0284; S00758; I37628; B32933; A31460
R;Ravetch, J.V.; Perussia, B.
J. Exp. Med. 170, 481-497, 1989
A;Title: Alternative membrane forms of Fc gamma RIII(CD16) on human natural killer cells
A;Reference number: JL0107; MUID:89328325; PMID:2526846
A;Accession: JU0284
A;Molecule type: mRNA
A;Residues: 1-201,'SF',204-233 <RAV>
A;Cross-references: GB:J04162
A;Note: the sequence of the receptor from human NK cells, reported in the same paper, di
rboxyl end
R;Simmons, D.; Seed, B.
Nature 333, 568-570, 1988
A;Title: The Fc-gamma receptor of natural killer cells is a phospholipid-linked membrane
A;Reference number: S00758; MUID:88232937; PMID:2967436
A;Accession: S00758
A;Molecule type: mRNA
A;Residues: 1-233 <SIM>
A;Cross-references: EMBL:X07934; NID:g29744; PIDN:CAA30758.1; PID:g29745
R;Gessner, J.E.; Grussenmeyer, T.; Kolanus, W.; Schmidt, R.E.
J. Biol. Chem. 270, 1350-1361, 1995
A;Title: The human low affinity immunoglobulin G Fc receptor III-A and III-B genes. Mole
A;Reference number: A55439; MUID:95138131; PMID:7836402
A;Accession: I37628
A;Molecule type: DNA
A;Residues: 1-72 <RES>
A;Cross-references: EMBL:Z46223; NID:g559446; PIDN:CAA86296.1; PID:g871306
R;Scallon, B.J.; Scigliano, E.; Freedman, V.H.; Miedel, M.C.; Pan, Y.C.E.; Unkeless, J.C
Proc. Natl. Acad. Sci. U.S.A. 86, 5079-5083, 1989
A;Title: A human immunoglobulin G receptor exists in both polypeptide-anchored and phosp
A;Reference number: A32933; MUID:89296947; PMID:2525780
A;Accession: B32933
A;Molecule type: mRNA
A;Residues: 1-121,'E',123-150,'S',152-233 <SCA>
A;Cross-references: GB:M24854; NID:g184851; PIDN:AAA53507.1; PID:g306930
R;Peltz, G.A.; Grundy, H.O.; Lebo, R.V.; Yssel, H.; Barsh, G.S.; Moore, K.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 1013-1017, 1989
A;Title: Human Fc-gamma-RIII: cloning, expression, and identification of the chromosomal
A;Reference number: A31460; MUID:89128838; PMID:2521732
A;Accession: A31460
A;Molecule type: mRNA
A;Residues: 1-35,'R',37-64,'N',66-81,'D',83-105,'V',107-233 <PEL>
A;Cross-references: GB:J04162; NID:g183036; PIDN:AAA35881.1; PID:g183037
C;Comment: This low affinity IgG Fc receptor of neutrophils, which is the product of the
l, yet this receptor lacks 21 residues at the carboxyl end because of an early stop codc
C;Genetics:
A;Gene: GDB:FCGR3B; FCG3; FCGR3
A;Cross-references: GDB:128176; OMIM:146740
A;Map position: 1q23-1q23
A;Introns: 14/1; 21/1
A;Note: the list of introns is incomplete
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: blocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkag
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-203/Product: Fc gamma (IgG) receptor III-B #status predicted <MAT>
F;40-91/Domain: immunoglobulin homology <IMM1>
F;111-174/Domain: immunoglobulin homology <IMM2>
F;56,63,82,92,180,187/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;203/Modified site: GPI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form

  Query Match 29.2%; Score 406; DB 1; Length 233;
  Best Local Similarity 40.4%; Pred. No. 3.5e-24;
  Matches 93; Conservative 33; Mismatches 94; Indels 10; Gaps 3;

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Qy         10 LLCVALLFFAPDGVLAVPQKPK--VSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHN 67
              ||  |||     | :    ||  | | | |  : : ::||| | |    | :||:||||
Db          5 LLPTALLLLVSAG-MRTEDLPKAVVFLEPQWYSVLEKDSVTLKCQGAYSPEDNSTQWFHN 63
```

```
Qy          68 GSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQP 127
               ||       ||  |  |   |||||:||      |:|| |||   ||||||   |  | |
Db          64 ESLISSQASSYFIDAATVNDSGEYRCQTNLSTLSDPVQLEVHIGWLLLQAPRWVFKEEDP 123

Qy         128 LFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYES 187
               : |||| |:|  ::|| | ::|:  ||:: | :  |  ||:|||:|:| | |   :  |
Db         124 IHLRCHSWKNTALHKVTYLQNGKDRKYFHHNSDFHIPKATLKDSGSYFCRGLVGSKNVSS 183

Qy         188 EPLNITVIKAPREKYWLQFFIP-------LLVVILFAVDTGLFISTQQQV 230
               | :|||: :          |  |       |::|:||||||||: | :  :
Db         184 ETVNITITQGLAVSTISSFSPPGYQVSFCLVMVLLFAVDTGLYFSVKTNI 233


RESULT 6
I46021
Fc-gamma receptor II - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 23-Jul-1999
C;Accession: I46021; S40204
R;Zhang, G.; Young, J.R.; Tregaskes, C.R.; Howard, C.J.
Immunogenetics 39, 423-427, 1994
A;Title: Cattle Fc gamma RII: molecular cloning and ligand specificity.
A;Reference number: I46021; MUID:94245284; PMID:8188320
A;Accession: I46021
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-296 <ZHA>
A;Cross-references: EMBL:X75671; NID:g437978; PIDN:CAA53367.1; PID:g437979
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: immunoglobulin receptor

  Query Match             29.1%;  Score 405;  DB 2;  Length 296;
  Best Local Similarity   42.2%;  Pred. No. 5.4e-24;
  Matches   79;  Conservative   33;  Mismatches   71;  Indels    4;  Gaps    2;

Qy          10 LLCVALLFFAPDGVLAVPQKPK--VSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHN 67
               ||  |||| ||  |   |  ||  |:: | |  : : ::|||| | :|   : | ||||
Db          29 LLWTALLFLAP--VSGKPDLPKAVVTIQPAWINVLREDHVTLTCQGTSFSAGNLTTWFHN 86

Qy          68 GSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQP 127
               ||            |   ||| |:|| :| : |:||:|:| |||||||  : |  ||:|
Db          87 GSSIHTQKQPSYSFRAGSNDSGSYRCQREQTSLSDPVHLDVISDWLLLQTPSLVFQEGEP 146

Qy         128 LFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYES 187
               : |||| |||  : |: :|:| ::  : |:  | ||  | :  || |:||  : :: : |
Db         147 IMLRCHSWRNQPLNKITFYQDRKSKIFSYQRTNFSIPRANLSHSGQYHCTAFIGKMLHSS 206

Qy         188 EPLNITV 194
               :|:||||
Db         207 QPVNITV 213


RESULT 7
I55577
Fc gamma (IgG) receptor I-B splice form 1 precursor - human
N;Alternate names: CD64
N;Contains: Fc-gamma (IgG) receptor I-B splice form 2
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I55577; I70303
R;Porges, A.J.; Redecha, P.B.; Doebele, R.; Pan, L.C.; Salmon, J.E.; Kimberly, R.P.
J. Clin. Invest. 90, 2102-2109, 1992
A;Title: Novel Fc gamma receptor I family gene products in human mononuclear cells.
A;Reference number: I55577; MUID:93055454; PMID:1430234
A;Accession: I55577
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-280 <RES>
A;Cross-references: GB:L03419; NID:g182460; PIDN:AAA35825.1; PID:g292023
A;Note: splice form B1
A;Accession: I70303
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-10,103-153,'A',155-280 <RE2>
A;Cross-references: GB:L03420; NID:g182461; PIDN:AAA35826.1; PID:g292024
A;Experimental source: mononuclear cells
A;Note: splice form B2
C;Comment: This receptor does not bind monomeric IgG with high affinity.
C;Genetics:
A;Gene: GDB:FCGR1B; CD64
A;Cross-references: GDB:135923; OMIM:601502
A;Map position: 1p12-1p12
C;Superfamily: Fc gamma receptor I; immunoglobulin homology
C;Keywords: alternative splicing; glycoprotein; immunoglobulin receptor; transmembrane p
F;117-170/Domain: immunoglobulin homology <IMM>

  Query Match             29.0%;  Score 403;  DB 2;  Length 280;
  Best Local Similarity   36.1%;  Pred. No. 7.3e-24;
  Matches   84;  Conservative   50;  Mismatches   89;  Indels   10;  Gaps    4;

Qy          11 LCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSL 70
               |  ||:  || :   |  ::| |||  :|: | ||| |   :    |||:|| ||:
Db           4 LTTLLLWVPVDGQVDT-TKAVITLQPPWVSVFQEETVTLHCEVLHLPGSSSTQWFLNGTA 62

Qy          71 SEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFL 130
               :: :  |  | :|   |||||:||       |:|: ||:   ||||| |: | |||:|| |
Db          63 TQTSTPSYRITSASVNDSGEYRCQRGLSGRSDPIQLEIHRGWLLLQVSSRVFMEGEPLAL 122

Qy         131 RCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPL 190
               ||| |::  || |:||:|:| |::: | |::|    :  :|||:|:| : :  | |  :
Db         123 RCHAWKDKLVYNVLYYRNGKAFKFFHWNSNLTILKTNISHNGTYHCSG-MGKHRYTSAGI 181

Qy         191 NITVIKAPR--EKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRK 241
               :  :|  :      |       | | |:| |:|  |::: :::      :|| :|
Db         182 SQYTVKGLQLPTPVWFHVLFYLAVGIMFLVNTVLWVTIRKE------LKRKKK 228


RESULT 8
S29360
Fc gamma (IgG) receptor alpha - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S29360; S46999
R;Ravetch, J.V.; Luster, A.D.; Weinshank, R.; Kochan, J.; Pavlovec, A.; Portnoy, D.A.; H
Science 234, 718-725, 1986
A;Title: Structural heterogeneity and functional domains of murine immunoglobulin G Fc r
A;Reference number: S29360; MUID:87042761; PMID:2946078
A;Accession: S29360
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <RAV>
A;Cross-references: EMBL:M14215; NID:g193247; PIDN:AAA37604.1; PID:g309228
R;Feinman, R.; Qiu, W.Q.; Pearse, R.N.; Nikolajczyk, B.S.; Sen, R.; Sheffery, M.; Ravetc
EMBO J. 13, 3852-3860, 1994
A;Title: PU.1 and an HLH family member contribute to the myeloid-specific transcription
A;Reference number: S46999; MUID:94349933; PMID:8070412
A;Accession: S46999
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-22 <FEI>
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: immunoglobulin receptor; transmembrane protein
F;130-183/Domain: immunoglobulin homology <IMM2>

  Query Match             28.9%;  Score 401.5;  DB 2;  Length 261;
  Best Local Similarity   35.6%;  Pred. No. 8.8e-24;
  Matches   90;  Conservative   44;  Mismatches  104;  Indels   15;  Gaps    5;

Qy          11 LCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNG-S 69
               | : |||   |.  |   |  | |:||| :: | : ||| | |  :    |||:||||| |
Db          16 LTILLLFAFADRQSAALPKAVVKLDPPWIQVLKEDMVTLMCEGTHNPGNSSTQWFHNGRS 75

Qy          70 LSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLF 129
               : :  :|    |  |||||:|| :|   |:|| | | |||||||    | :||: :
Db          76 IRSQVQASYTF-KATVNDSGEYRCQMEQTRLSDPVDLGVISDWLLLQTPQRVFLEGETIT 134
```

```
Qy        130 LRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEP 189
              |||| ||| : :: :: : ::::| :   | || |    || ||| | :    ::|:|
Db        135 LRCHSWRNKLLNRISFFHNEKSVRYHHYKSNFSIPKANHSHSGDYYCKGSLGSTQHQSKP 194

Qy        190 LNITV----IKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFR- 244
              : |||      :     |      |:: :||||||||:   ::       ::  |: :|
Db        195 VTITVQDPATTSSISLVWYHTAFSLVMCLLFAVDTGLYFYVRR------NLQTPREYWRK 248

Qy        245 --LLNPHPKPNPK 255
                :  |  |  |
Db        249 SLSIRKHQAPQDK 261
```

RESULT 9
I56110
Fc-gamma RIIIB-alpha - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jan-2000
C;Accession: I56110
R;Farber, D.L.; Sears, D.W.
J. Immunol. 146, 4352-4361, 1991
A;Title: Rat Cd16 is defined by a family of class III Fc-gamma receptors requiring co-ex
A;Reference number: I56110; MUID:91250730; PMID:1710249
A;Accession: I56110
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-267 <RES>
A;Cross-references: GB:M64369; NID:g206674; PIDN:AAA42048.1; PID:g206675
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
F;55-106/Domain: immunoglobulin homology <IMM>

  Query Match 28.7%; Score 399; DB 2; Length 267;
  Best Local Similarity 37.1%; Pred. No. 1.4e-23;
  Matches 83; Conservative 42; Mismatches 95; Indels 4; Gaps 1;

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Qy         11 LCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSL 70
              | : |||    |    |    |  | :||| :: | : ||||| | :     |||:|||| |
Db         22 LTMLLLFAFADRQTANLPKAVVKRDPPWIQVLKEDTVTLTCEGTHNPGNSSTQWFHNQSS 81

Qy         71 SEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFL 130
              :      :     |   |||||:|:    : |:|::||| |||||||     |  ||: : |
Db         82 TWGQVQASYTFKATVNDSGEYRCRMAHTSLSDPIHLEVISDWLLLQTPQLVFEEGETITL 141

Qy        131 RCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPL 190
              ||| |:|  : ||: :::|: ::|:|:: | ||  |    || |||   : :  : |:|:
Db        142 RCHSWKNKQLTKVLLFQNGKPVRYYYQSSNFSIPKANHSHSGNYYCKAYLGRTMHVSKPV 201

Qy        191 NITV----IKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQV 230
              |||      :     |      |:: :||||||||:   :: :
Db        202 TITVQGSATASTSSLVWFHAAFCLVMCLLFAVDTGLYFCVRRNL 245
```

RESULT 10
A35902
Fc gamma (IgG) receptor II (low affinity) alpha precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999
C;Accession: A35902
R;Zeger, D.L.; Hogarth, P.M.; Sears, D.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 3425-3429, 1990
A;Title: Characterization and expression of an Fc-gamma receptor cDNA cloned from rat na
A;Reference number: A35902; MUID:90239026; PMID:1692135
A;Accession: A35902
A;Molecule type: mRNA
A;Residues: 1-267 <ZEG>
A;Cross-references: GB:M32062; NID:g204114; PIDN:AAA41148.1; PID:g204115
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: duplication; glycoprotein; immunoglobulin receptor; transmembrane protein
F;55-106/Domain: immunoglobulin homology <IMM>

  Query Match 28.4%; Score 395; DB 2; Length 267;
  Best Local Similarity 36.6%; Pred. No. 2.9e-23;
  Matches 82; Conservative 42; Mismatches 96; Indels 4; Gaps 1;

```
Qy         11 LCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSL 70
              | : |||    |    |    |  | :||| :: | : ||||| | :     |||:|||| |
Db         22 LTMLLLFAFADRQTGDLLKAVVKRDPPWIQVLKDDTVTLTCEGTHNPGNSSTQWFHNQSS 81

Qy         71 SEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFL 130
              :      :     |   |||||:|:    : |:|::||| |||||||     |  ||: : |
Db         82 TWGQVQASYTFKATVNDSGEYRCRMAHTSLSDPIHLEVISDWLLLQTPQLVFEEGETITL 141

Qy        131 RCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPL 190
              ||| |:|  : ||: :::|: ::|:|:: | ||  |    || |||   : :  : |:|:
Db        142 RCHSWKNKQLTKVLLFQNGKPVRYYYQSSNFSIPKANHSHSGNYYCKAYLGRTMHVSKPV 201

Qy        191 NITV----IKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQV 230
              |||      :     |      |:: :||||||||:   :: :
Db        202 TITVQGSATASTSSLVWFHAAFCLVMCLLFAVDTGLYFCVRRNL 245
```

RESULT 11
A34636
Fc-gamma receptor II precursor - guinea pig
C;Species: Cavia porcellus (guinea pig)
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 16-Jul-1999
C;Accession: A34636
R;Tominaga, M.; Sakata, A.; Ohmura, T.; Yamashita, T.; Koyama, J.; Onoue, K.
Biochem. Biophys. Res. Commun. 168, 683-689, 1990
A;Title: The structure and expression of the guinea pig Fc receptor for IgG1 and IgG2 (h
A;Reference number: A34636; MUID:90241239; PMID:1692213
A;Accession: A34636
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-270 <TOM>
A;Cross-references: GB:M35272
C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: immunoglobulin receptor
F;37-88/Domain: immunoglobulin homology <IMM>

  Query Match 28.1%; Score 390.5; DB 2; Length 270;
  Best Local Similarity 36.7%; Pred. No. 6.4e-23;
  Matches 88; Conservative 37; Mismatches 108; Indels 7; Gaps 4;

```
Qy         10 LLCVALLFFAP-DGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNG 68
              || : :|| ||  |  | | |  | | ||| :: :|: ||||| |       ||:| |||
Db          2 LLWITVLFLAPVAGTSADPPKAVVRLEPPWIQVLRGDRVTLTCEGAPSPGNHSTQWLHNG 61

Qy         69 SLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPL 128
              |              ||  |||||:||    : |:|| |:| ||||:|| |  :  ||  :
Db         62 RLIPTQVLPSYRFTAKGNDSGEYRCQAGGTSLSDPVRLDVISDWLVLQTSQLIFQEGDVI 121

Qy        129 FLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESE 188
              |||| | || : || :| :| | | ||:  : | ||  |    || | ||| : :  : |
Db        122 VLRCHSWNNWPLAKVTFYHNGVAKKYFSISKNFSIPQANHSHSGAYNCTGLIGRTSHTSP 181

Qy        189 PLNITVIKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNP 248
              |: ||| : |:      : ::|  :  : |   :    .  |  :: :|: :    | :|
Db        182 PVTITV-QGPKSSD--SSMVVIIVAAVIGIATAAIVVA---VVAIICLKKKQPPANLSDP 235
```

RESULT 12
I72882
Fc gamma receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: I72882
R;Sears, D.
J. Immunol. 150, 4364-4375, 1993
A;Title: Rat class III Fc gamma receptor isoforms differ in IgG subclass-binding specifi
A;Reference number: I56166; MUID:93246650; PMID:8482840
A;Accession: I72882
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-267 <RES>
A;Cross-references: GB:L08446; NID:g204120; PIDN:AAA41151.1; PID:g204121

C;Superfamily: Fc gamma receptor III; immunoglobulin homology
C;Keywords: immunoglobulin receptor
F;55-106/Domain: immunoglobulin homology <IMM>

Query Match 27.3%; Score 380; DB 2; Length 267;
Best Local Similarity 36.2%; Pred. No. 4.1e-22;
Matches 81; Conservative 43; Mismatches 96; Indels 4; Gaps 1;

```
Qy          11 LCVALLFPAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSL 70
               | : |||    |      |  |  :||| :: | : ||||| | :    |||:|||| |
Db          22 LTMLLLFAFADRQTGDLLKAVVKRDPPWIQVLKDDTVTLTCEGTHNPGNSSTQWFHNQSS 81

Qy          71 SEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFL 130
               :     :     |   |||||:|:    : |:||:||| |||||||    | :||: : |
Db          82 TWGQVQASYTFKATVNDSGEYRCRMAHTSLSDPVHLEVISDWLLLQTPQLVFLEGERITL 141

Qy         131 RCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPL 190
               |||||::  : :: : ::|| : :   | : ||:||    || |||   : : :: |:|:
Db         142 RCHGWKSIQLARISFLQNGEFVSFHPYNVSYSISNANHSHSGDYYCKAYLGRTEHVSKPV 201

Qy         191 NITV----IKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQV 230
                |||      :     |      |:: :||||||||:   :: :
Db         202 TITVQQGSATASTSSLVWFHAAFCLVMCLLFAVDTGLYFCVRRNL 245
```

RESULT 13
I48471
Fc gamma (IgG) receptor high affinity - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I48471
R;Prins, J.B.; Todd, J.A.; Rodrigues, N.R.; Ghosh, S.; Hogarth, P.M.; Wicker, L.S.; Gaff
Science 260, 695-698, 1993
A;Title: Linkage on chromosome 3 of autoimmune diabetes and defective Fc receptor for Ig
A;Reference number: I48471; MUID:93242399; PMID:8480181
A;Accession: I48471
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-336 <RES>
A;Cross-references: EMBL:X70980; NID:g311748; PIDN:CAA50311.1; PID:g311749
C;Superfamily: Fc gamma receptor I; immunoglobulin homology
C;Keywords: immunoglobulin receptor
F;128-180/Domain: immunoglobulin homology <IMM>

Query Match 27.3%; Score 379; DB 2; Length 336;
Best Local Similarity 37.8%; Pred. No. 6.3e-22;
Matches 90; Conservative 42; Mismatches 94; Indels 12; Gaps 6;

```
Qy          10 LLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGS 69
               ||    ||:     | :     |  ::| |||  ||: ||||| | | :    |||:|| ||:
Db          12 LLTTLLLWVPVGGEVVNATKAVITLQPPWASIFQKENVTLWCEGPHLPGDSSTQWFINGT 71

Qy          70 LSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVF-SDWLLLQASAEVVMEGQPL 128
               : : :  | :|   | |:|||||:||       |:|| |::   ||||||||  |: ||:||
Db          72 VVQTSTPSYSISVASFQDSGEYRCQIGSSVPSDPVQLQIHKEDWLLLQASRRVLTEGEPL 131

Qy         129 FLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESE 188
               ||||||:|  || |::|::|:: |:       |:|    :  || |:|:| : :  | |
Db         132 ALRCHGWKNKLVYNVVFYRNGKSFKF-SSGSKIAILKTNLSHSGIYHCSG-MGRHRYTSA 189

Qy         189 PLNITVIKAPREKYWLQFFIPLL-VVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRL 245
               ::|||   | |     |  |:|   :       | ::   :   ||:    | | :|
Db         190 GVSITVKAPPLE----LFTTPVLRASVSSPFPEGSLVTLNCETNLLLQ----RPGLQL 239
```

RESULT 14
A46480
Fc gamma (IgG) receptor high affinity - mouse
N;Alternate names: high affinity IgG receptor
C;Species: Mus musculus (house mouse)
C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C;Accession: A46480; A43511
R;Osman, N.; Kozak, C.A.; McKenzie, I.F.; Hogarth, P.M.
J. Immunol. 148, 1570-1575, 1992
A;Title: Structure and mapping of the gene encoding mouse high affinity Fc gamma RI and
A;Reference number: A46480; MUID:92166399; PMID:1531670
A;Accession: A46480
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-404 <OSM>
A;Note: sequence extracted from NCBI backbone (NCBIN:85205, NCBIN:85208, NCBIN:85212, NC
R;Sears, D.W.; Osman, N.; Tate, B.; McKenzie, I.F.C.; Hogarth, P.M.
J. Immunol. 144, 371-378, 1990
A;Title: Molecular cloning and expression of the mouse high affinity Fc receptor for IgG
A;Reference number: A43511; MUID:90111035; PMID:2136886
A;Accession: A43511
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-404 <SEA>
A;Cross-references: GB:M31314; NID:g200752; PIDN:AAA40056.1; PID:g200753
C;Superfamily: Fc gamma receptor I; immunoglobulin homology
C;Keywords: immunoglobulin receptor; transmembrane protein
F;127-179/Domain: immunoglobulin homology <IMM>

Query Match 27.3%; Score 379; DB 2; Length 404;
Best Local Similarity 41.6%; Pred. No. 7.8e-22;
Matches 77; Conservative 37; Mismatches 69; Indels 2; Gaps 2;

```
Qy          10 LLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGS 69
               ||    ||:     | :     |  ::| |||  ||: ||||| | | :    |||:|| ||:
Db          12 LLTTLLLWVPVGGEVVNATKAVITLQPPWVSIFQKENVTLWCEGPHLPGDSSTQWFINGT 71

Qy          70 LSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLF 129
                 : :  | :|   | |:|||||:||       |:|| |:: :|||||||  |: ||:||
Db          72 AVQISTPSYSIPEASFQDSGEYRCQIGSSMPSDPVQLQIHNDWLLLQASRRVLTEGEPLA 131

Qy         130 LRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEP 189
               ||||||:|  || |::|::|:: ::   :  ::|    :  || |:|:|   :  | |
Db         132 LRCHGWKNKLVYNVVFYRNGKSFQF-SSDSEVAILKTNLSHSGIYHCSG-TGRHRYTSAG 189

Qy         190 LNITV 194
               ::|||
Db         190 VSITV 194
```

RESULT 15
A41357
Fc gamma (IgG) receptor I (high affinity) form b - human
N;Alternate names: CD64
C;Species: Homo sapiens (man)
C;Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 21-Jan-2000
C;Accession: A41357; S03019
R;Allen, J.M.; Seed, B.
Science 243, 378-381, 1989
A;Title: Isolation and expression of functional high-affinity Fc receptor complementary
A;Reference number: A41357; MUID:89100284; PMID:2911749
A;Accession: A41357
A;Molecule type: mRNA
A;Residues: 1-344 <ALL1>
A;Cross-references: GB:X14355; GB:M21090; NID:g31333; PIDN:CAA32536.1; PID:g31334
R;Allen, J.M.; Seed, B.
Nucleic Acids Res. 16, 11824, 1988
A;Title: Nucleotide sequence of three cDNAs for the human high affinity Fc receptor (FcR
A;Reference number: S03018; MUID:89098339; PMID:2974947
A;Accession: S03019
A;Molecule type: mRNA
A;Residues: 1-344 <ALL2>
A;Cross-references: EMBL:X14355; NID:g31333; PIDN:CAA32536.1; PID:g31334
A;Note: the authors translated the codon ACT for residue 25 as Ala
C;Superfamily: Fc gamma receptor I; immunoglobulin homology
C;Keywords: alternative splicing; immunoglobulin receptor; transmembrane protein
F;117-170/Domain: immunoglobulin homology <IMM>

Query Match 27.1%; Score 376; DB 2; Length 344;
Best Local Similarity 39.7%; Pred. No. 1.1e-21;
Matches 73; Conservative 39; Mismatches 70; Indels 2; Gaps 2;

```
Qy          11 LCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSL 70
               |   ||:   || :    |  ::| |||  :|: | ||| |   :    |||:|| ||: 
Db           4 LTTLLLWVPVDGQVDT-TKAVITLQPPWVSVFQEETVTLHCEVLHLPGSSSTQWFLNGTA 62

Qy          71 SEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFL 130
               :: :  |  | :|   |||||:||      |:|: ||:   ||||| |: |  ||:|| |
Db          63 TQTSTPSYRITSASVNDSGEYRCQRGLSGRSDPIQLEIHRGWLLLQVSSRVFTEGEPLAL 122

Qy         131 RCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPL 190
               ||| |::  || |:||::|:| |::: | |::|    :  :|||:|:| : :  | |  :
Db         123 RCHAWKDKLVYNVLYYRNGKAFKFFHWNSNLTILKTNISHNGTYHCSG-MGKHRYTSAGI 181

Qy         191 NITV 194
               ::||
Db         182 SVTV 185
```

Search completed: October 6, 2004, 09:23:41
Job time : 16.0781 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:40 ; Search time 40.4371 Seconds
(without alignments)
2005.293 Million cell updates/sec

Title: US-10-763-400-2
Perfect score: 1390
Sequence: 1 MAPAMESPTLLCVALLFFAP.....RTRKGFRLLNPHPKPNPKNN 257

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	832.5	59.9	255	6	Q8MI30	Q8mi30 equus cabal
2	800	57.6	260	6	Q8MJZ0	Q8mjz0 ovis aries
3	419	30.1	254	6	Q8SPW2	Q8spw2 macaca fasc
4	411	29.6	249	6	Q9N2I6	Q9n2i6 felis silve
5	405.5	29.2	250	6	Q9N2I5	Q9n2i5 felis silve
6	403.5	29.0	256	6	Q95N22	Q95n22 sus scrofa
7	403	29.0	280	4	Q92637	Q92637 homo sapien
8	402	28.9	233	4	Q9UPY7	Q9upy7 homo sapien
9	401.5	28.9	249	11	Q8R477	Q8r477 mus musculu
10	399.5	28.7	249	11	Q8R2R4	Q8r2r4 mus musculu
11	398	28.6	261	11	Q9ES92	Q9es92 mus musculu
12	386	27.8	261	11	Q7TMW9	Q7tmw9 mus musculu
13	383.5	27.6	357	6	Q8SPW5	Q8spw5 macaca fasc
14	380.5	27.4	294	6	Q8SPW3	Q8spw3 macaca fasc
15	379	27.3	330	11	Q8R142	Q8r142 mus musculu
16	378.5	27.2	349	6	Q9MZT0	Q9mzt0 bos taurus
17	376	27.1	374	4	Q92663	Q92663 homo sapien
18	375.5	27.0	375	4	Q92495	Q92495 homo sapien
19	366.5	26.4	372	6	Q7YQJ5	Q7yqj5 canis famil
20	366	26.3	227	6	Q95N21	Q95n21 sus scrofa
21	355	25.5	318	11	Q8VIQ0	Q8viq0 rattus norv
22	352	25.3	310	6	Q8SPW4	Q8spw4 macaca fasc
23	351	25.3	316	6	Q8SPV8	Q8spv8 pan troglod
24	341.5	24.6	316	4	Q8WW64	Q8ww64 homo sapien
25	337.5	24.3	316	4	Q8WUN1	Q8wun1 homo sapien
26	271.5	19.5	515	4	Q96RE0	Q96re0 homo sapien
27	269.5	19.4	199	4	Q96P27	Q96p27 homo sapien
28	269.5	19.4	639	4	Q96P30	Q96p30 homo sapien
29	268.5	19.3	734	4	Q96P31	Q96p31 homo sapien
30	268.5	19.3	734	4	Q96LA4	Q96la4 homo sapien
31	268.5	19.3	740	4	Q96P29	Q96p29 homo sapien
32	268.5	19.3	742	4	Q8N6S2	Q8n6s2 homo sapien
33	267.5	19.2	189	4	Q96P28	Q96p28 homo sapien
34	267.5	19.2	515	4	Q96PJ5	Q96pj5 homo sapien
35	267	19.2	977	4	Q96RD9	Q96rd9 homo sapien
36	257	18.5	582	11	Q80WN2	Q80wn2 mus musculu
37	246	17.7	360	4	Q8N732	Q8n732 homo sapien
38	232.5	16.7	188	4	Q92638	Q92638 homo sapien
39	206	14.8	509	11	Q91YK7	Q91yk7 mus musculu
40	206	14.8	509	11	Q9EQY5	Q9eqy5 mus musculu
41	194.5	14.0	168	6	Q9N1Y3	Q9n1y3 bos taurus
42	191.5	13.8	130	4	Q8IZV7	Q8izv7 homo sapien
43	187.5	13.5	365	4	Q8NEW4	Q8new4 homo sapien
44	187.5	13.5	376	4	Q8WXH3	Q8wxh3 homo sapien
45	175.5	12.6	352	11	Q920A9	Q920a9 mus musculu

ALIGNMENTS

RESULT 1
Q8MI30
ID Q8MI30 PRELIMINARY; PRT; 255 AA.
AC Q8MI30;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE High affinity immunoglobulin E receptor alpha subunit.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1; TISSUE=Bronchoalveolar lavage fluid;
RX MEDLINE=20424522; PubMed=10970105;
RA McAleese S.M., Halliwell R.E.W., Miller H.R.P.;
RT "Cloning and Sequencing of the horse and sheep high-affinity IgE
RT receptor alpha chain cDNA.";
RL Immunogenetics 51:878-881(2000).
DR EMBL; Y18204; CAB40387.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00408; IGc2; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 255 AA; 29366 MW; A60659700684FBD8 CRC64;

Query Match 59.9%; Score 832.5; DB 6; Length 255;
Best Local Similarity 63.9%; Pred. No. 4.9e-67;
Matches 163; Conservative 31; Mismatches 56; Indels 5; Gaps 2;

Qy 1 MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVS 60
Db 1 MPAPMGSPALLWITFLLFSLDGVPAAIRKSTVSLNPPWNRIFRGENVTLTCNKNKPLKGN 60

```
Qy         61 STKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAE 120
              ||:| :| :  | | ||||| ||    ||||:|::  :| || |:|||||||||||||||
Db         61 STEWTYNNTTLEVTTSSLNITNASHRSSGEYRCRNNDLNLSEAVHLEVFSDWLLLQASAE 120

Qy        121 VVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTG-- 178
               |:||: | ||| ||::|||:||||||||: |:||||| |||| :|| |:|||||| |
Db        121 EVIEGKALVLRCRGWKDWDVFKVIYYKDGKPLEYWYENKNISIESATTENSGTYYCEGAF 180

Qy        179 --KVWQLDYESEPLNITVIKAPREK-YWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLK 235
                 |    | |: ||||| || : | ||||| |||||||||||||||:|||||:|||||
Db        181 NFKRTSERYTSDYLNITVKKAEQSKRYWLQFIIPLLVVILFAVDTGLFVSTQQQLTFLLK 240

Qy        236 IKRTRKGFRLLNPHP 250
              |||||:| :|::|||
Db        241 IKRTRRGRKLMDPHP 255


RESULT 2
Q8MJZ0
ID   Q8MJZ0      PRELIMINARY;      PRT;   260 AA.
AC   Q8MJZ0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   High affinity immunoglobulin E receptor alpha subunit.
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=1; TISSUE=Bone marrow;
RX   MEDLINE=20424522; PubMed=10970105;
RA   McAleese S.M., Halliwell R.E.W., Miller H.R.P.;
RT   "Cloning and Sequencing of the horse and sheep high-affinity IgE
RT   receptor alpha chain cDNA.";
RL   Immunogenetics 51:878-881(2000).
DR   EMBL; Y18205; CAB40544.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   SMART; SM00408; IGc2; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Immunoglobulin domain; Receptor.
SQ   SEQUENCE   260 AA;  30047 MW;  67111F2F17D596ED CRC64;

  Query Match             57.6%;  Score 800;  DB 6;  Length 260;
  Best Local Similarity   60.0%;  Pred. No. 4.3e-64;
  Matches  153;  Conservative   31;  Mismatches   69;  Indels    2;  Gaps    1;

Qy          5 MESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKW 64
              | :| || :||| |:|||: |   | |||||||  ||:|| |||||  |    |  |: |
Db          6 MGAPALLWIALLLFSPDGMSAANWKSKVSLNPPWREIFRGETVTLTCGVNRSSENESSVW 65

Qy         65 FHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVME 124
               |||:  :|||| :|| |: :|||:|:|: :    |||||| | ||||:|||||||:||
Db         66 IHNGTTLKETNSRWDIVKARVQDSGKYQCRIKGFAISEPVYLNVISDWLILQASAEVMME 125

Qy        125 GQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLD 184
              |: |||||| |:| : :|||||||  |||||||||||||||| |  ||| ||| |:: :|:
Db        126 GESLFLRCHSWKNLNAFKVIYYKDNRALKYWYENHNISITNVTEGDSGIYYCVGRIQRLN 185

Qy        185 YESEPLNITVIKAPREK--YWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKG 242
              | |  | | | |   :   :|||| |||||:||| ||||| |||||| | |||:|| ||
Db        186 YTSNKLKIIVKKQYTQSNYFWLQFLIPLLVLILFVVDTGLLISTQQQFTLLLKMKRIRKR 245

Qy        243 FRLLNPHPKPNPKNN 257
               |  :| |||:|  |
Db        246 NRFTDPQPKPDPPGN 260


RESULT 3
Q8SPW2
ID   Q8SPW2      PRELIMINARY;      PRT;   254 AA.
AC   Q8SPW2;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fc gamma receptor IIIa.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Namenuk A.K., Hong K., Meng Y.G., Shields R.L., Cromwell M.E.M.,
RA   Presta L.G.;
RT   "Binding of human IgG to cynomolgus FcR.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF485815; AAL92098.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Receptor.
SQ   SEQUENCE   254 AA;  29120 MW;  11A48E6B3A34AF7B CRC64;

  Query Match             30.1%;  Score 419;  DB 6;  Length 254;
  Best Local Similarity   40.4%;  Pred. No. 1e-29;
  Matches   93;  Conservative   39;  Mismatches   88;  Indels   10;  Gaps    3;

Qy         10 LLCVALLFFAPDGVLA--VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHN 67
              ||  |||     |: |  :| |  | | | | |: : : ||| | |    | :||:||||
Db          5 LLPTALLLLVSAGMRAEDLP-KAVVFLEPQWYRVLEKDRVTLKCQGAYSPEDNSTRWFHN 63

Qy         68 GSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQP 127
               ||      ||  |  |:  :||||:||      |:|| |||   ||||||   | | :
Db         64 ESLISSQTSSYFIAAARVNNSGEYRCQTSLSTLSDPVQLEVHIGWLLLQAPRWVFKEEES 123

Qy        128 LFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYES 187
              : |||| |:|  ::|| | ::|:  ||:::| :  |  ||::|||:|:| | :   :  |
Db        124 IHLRCHSWKNTLLHKVTYLQNGKGRKYFHQNSDFYIPKATLKDSGSYFCRGLIGSKNVSS 183

Qy        188 EPLNITVIKAPREKYWLQFFIP-------LLVVILFAVDTGLFISTQQQV 230
              | :|||: :          || |       |::|:|||||||: | :: :
Db        184 ETVNITITQDLAVSSISSFFPPGYQVSFCLVMVLLFAVDTGLYFSMKKSI 233


RESULT 4
Q9N2I6
ID   Q9N2I6      PRELIMINARY;      PRT;   249 AA.
AC   Q9N2I6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD16.
GN   CD16.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20180233; PubMed=10713347;
RA   Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,
RA   Mikami T., Takahashi E.;
RT   "Molecular cloning and sequencing of the cDNA encoding the feline
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RT   Fc(gamma)RIIIA (CD16) homologue.";
RL   Vet. Immunol. Immunopathol. 73:353-359(2000).
DR   EMBL; AB025314; BAA92347.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   249 AA;  27902 MW;  683528C68A7CAB7A CRC64;

  Query Match             29.6%;  Score 411;  DB 6;  Length 249;
  Best Local Similarity   39.1%;  Pred. No. 5.4e-29;
  Matches   92;  Conservative   33;  Mismatches  100;  Indels   10;  Gaps    2;

Qy          7 SPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFH 66
              |||    |||      |  |   |  | | | |||:   : | | | |      :| :|:|
Db          6 SPT----ALLLLVSAGTRADLSKAMVVLEPEWNRVLVSDGVILKCEGAYPPGDNSAQWWH 61

Qy         67 NGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQ 126
              |||:      | :|  |: |||||||||      |:|| ||| : ||||||   |  ||
Db         62 NGSVIPHRAPSYSIEAARSEDSGEYKCQTGLSEASDPVQLEVHTGWLLLQAPRWVFQEGD 121

Qy        127 PLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYE 186
              :·|||| |:|  | || |::||    ::::| :  |  || : ||:|:| | :   :
Db        122 TIQLRCHSWKNKTVQKVQYFQDGRGKMFFHKNSDFYIPKATSKHSGSYFCRGLIGNKNES 181

Qy        187 SEPLNITVIKAPREK------YWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLK 235
              || :|||   |         :| |    |:  :|| ||||| :: |: :   :|
Db        182 SEAVNITVQGPPVPSTSTFLPHWYQIAFFLVTALLFVVDTGLHVAVQRDLQSSVK 236


RESULT 5
Q9N2I5
ID   Q9N2I5      PRELIMINARY;      PRT;   250 AA.
AC   Q9N2I5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD16.
GN   CD16.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20180233; PubMed=10713347;
RA   Nishimura Y., Miyazawa T., Ikeda Y., Izumiya Y., Nakamura K., Sato E.,
RA   Mikami T., Takahashi E.;
RT   "Molecular cloning and sequencing of the cDNA encoding the feline
RT   Fc(gamma)RIIIA (CD16) homologue.";
RL   Vet. Immunol. Immunopathol. 73:353-359(2000).
DR   EMBL; AB025315; BAA92348.1; -.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
SQ   SEQUENCE   250 AA;  27973 MW;  161350918A1628EB CRC64;

  Query Match             29.2%;  Score 405.5;  DB 6;  Length 250;
  Best Local Similarity   39.0%;  Pred. No. 1.7e-28;
  Matches   92;  Conservative   33;  Mismatches  100;  Indels   11;  Gaps    3;

Qy          7 SPTLLCVALLFFAPDGVLAVP-QKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWF 65
              |||    |||      |  |   |  | | | |||:   : | | | |      :| :|:
Db          6 SPT----ALLLLVSAGTRAADLSKAMVVLEPEWNRVLVSDGVILKCEGAYPPGDNSAQWW 61

Qy         66 HNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEG 125
              ||||:      | :|  |: |||||||||      |:|| ||| : ||||||   |  ||
Db         62 HNGSVIPHRAPSYSIEAARSEDSGEYKCQTGLSEASDPVQLEVHTGWLLLQAPRWVFQEG 121

Qy        126 QPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDY 185
              : |||| |:|  | || |::||    ::::| :  |  || : ||:|:| | :   :
Db        122 DTIQLRCHSWKNKTVQKVQYFQDGRGKMFFHKNSDFYIPKATSKHSGSYFCRGLIGNKNE 181

Qy        186 ESEPLNITVIKAPREK------YWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLK 235
              || :|||   |         :| |    |:  :|| ||||| :: |: :   :|
Db        182 SSEAVNITVQGPPVPSTSTFLPHWYQIAFFLVTALLFVVDTGLHVAVQRDLQSSVK 237


RESULT 6
Q95N22
ID   Q95N22      PRELIMINARY;      PRT;   256 AA.
AC   Q95N22;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   CD16A.a'.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Jie H.-B., Yim D., Kim Y.-S., Swanson T., Kim Y.B.;
RT   "Molecular Characterization of Porcine CD16 Isoforms.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF372453; AAK54249.1; -.
DR   GO; GO:0003677; F:DNA binding; IEA.
DR   GO; GO:0008170; F:N-methyltransferase activity; IEA.
DR   GO; GO:0006306; P:DNA methylation; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR002052; N6_Mtase.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
DR   PROSITE; PS00092; N6_MTASE; 1.
SQ   SEQUENCE   256 AA;  28868 MW;  B39D7D36DE39CF44 CRC64;

  Query Match             29.0%;  Score 403.5;  DB 6;  Length 256;
  Best Local Similarity   38.3%;  Pred. No. 2.7e-28;
  Matches   93;  Conservative   42;  Mismatches   89;  Indels   19;  Gaps    4;

Qy          7 SPTLLCVALLFFAPDGVLAV-PQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWF 65
              |||    |||      |  |   |  | |:|||:|: : ::||| | |       ||:|
Db          6 SPT----ALLLVSAGTHAEDPPKSVVILDPPWDRLLEKDSVTLKCQGAYPPGDDSTEWR 61

Qy         66 HNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEG 125
               ||:|      || :| :|    :|||| |:       :|:|: |||:  ||||||   || ||
Db         62 WNGTLISNKASSYSITDATVGNSGEYTCKTGLSAQSDPLRLEVYKGWLLLQAPRWVVQEG 121

Qy        126 QPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDY 185
              : : |||| |:|  : || |:::|    |: ::|     | |||::| |:|:| | :   :
Db        122 ESIRLRCHTWKNITIQKVQYFQNGMGKKFSHQNFEYHIPNATLKDGGSYFCRGIIKNYNL 181

Qy        186 ESEPLNITVIKAPREKYWLQFFIP-------LLVVILFAVDTGLFISTQQQVTFLLKIKR 238
               || : :||  :       | ||:|       |::  |||||||: | :       |: |
Db        182 SSEAVKVTVQGSKSPSPILSFFLPWHQIIFCLVMGFLFAVDTGLYFSVR-------KVLR 234

Qy        239 TRK 241
              : |
Db        235 SSK 237


RESULT 7
Q92637
ID   Q92637      PRELIMINARY;      PRT;   280 AA.
AC   Q92637;
DT   01-FEB-1997 (TrEMBLrel. 02, Created)
DT   01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fc gamma receptor I.
GN   B1.
OS   Homo sapiens (Human).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=93055454; PubMed=1430234;
RA   Porges A.J., Redecha P.B., Doebele R., Pan L.C., Salmon J.E.,
RA   Kimberly R.P.;
RT   "Novel Fc gamma receptor I family gene products in human mononuclear
RT   cells.";
RL   J. Clin. Invest. 90:2102-2109(1992).
DR   EMBL; L03419; AAA35825.1; -.
DR   PIR; I55577; I55577.
DR   GO; GO:0005886; C:plasma membrane; NAS.
DR   GO; GO:0003793; F:defense/immunity protein activity; NAS.
DR   GO; GO:0016489; F:immunoglobulin receptor activity; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Receptor.
SQ   SEQUENCE   280 AA;  32232 MW;  C6C6C45AE3D345C6 CRC64;

  Query Match             29.0%;  Score 403;  DB 4;  Length 280;
  Best Local Similarity   36.1%;  Pred. No. 3.3e-28;
  Matches   84;  Conservative   50;  Mismatches   89;  Indels   10;  Gaps    4;

Qy         11 LCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSL 70
              |    ||:   || :    |  ::| |||  :|: |.||| |   :    |||:|| ||:
Db          4 LTTLLLWVPVDGQVDT-TKAVITLQPPWVSVFQEETVTLHCEVLHLPGSSSTQWFLNGTA 62

Qy         71 SEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFL 130
              :: :  |  | :|   |||||:||      |:|: ||:   ||||| |: | |||:|| |
Db         63 TQTSTPSYRITSASVNDSGEYRCQRGLSGRSDPIQLEIHRGWLLLQVSSRVFMEGEPLAL 122

Qy        131 RCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPL 190
              ||| |::  || |:|::|:| |::: | |::|    :  :|||:|:| : :  | |  :
Db        123 RCHAWKDKLVYNVLYYRNGKAFKFFHWNSNLTILKTNISHNGTYHCSG-MGKHRYTSAGI 181

Qy        191 NITVIKAPR--EKYWLQFFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRK 241
              :   :|  :      |      | | |:| |:| |::: :::      :|| :|
Db        182 SQYTVKGLQLPTPVWFHVLFYLAVGIMFLVNTVLWVTIRKE------LKRKKK 228


RESULT 8
Q9UPY7
ID   Q9UPY7      PRELIMINARY;      PRT;   233 AA.
AC   Q9UPY7;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fc-gamma receptor IIIb (CD 16).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20487377; PubMed=11034564;
RA   Watanabe Y., Shimada E., Fujiwara K., Niihara H., Shimano K.,
RA   Mitsunaga S., Tadokoro K., Juji T.;
RT   "Nucleotide sequence of a new Fc gamma receptor IIIB allele that codes
RT   for a neutrophil antigen.";
RL   Tissue Antigens 56:272-275(2000).
DR   EMBL; AB025256; BAA83803.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 1.
KW   Receptor.
FT   VARIANT      54      54       K -> E.
SQ   SEQUENCE   233 AA;  26215 MW;  74B51B909272B388 CRC64;

  Query Match             28.9%;  Score 402;  DB 4;  Length 233;
  Best Local Similarity   40.0%;  Pred. No. 3.2e-28;
  Matches   92;  Conservative   34;  Mismatches   94;  Indels   10;  Gaps    3;

Qy         10 LLCVALLFFAPDGVLAVPQKPK--VSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHN 67
              ||  |||      | :     ||  | | | |  : : ::||| | |    : :||:||||
Db          5 LLPTALLLLVSAG-MRTEDLPKAVVFLEPQWYSVLEKDSVTLKCQGAYSPKDNSTQWFHN 63

Qy         68 GSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQP 127
              ||      ||  |  |  |||||:||       |:|| |||   ||||||   |  |  |
Db         64 ESLISSQASSYFIDAATVNDSGEYRCQTNLSTLSDPVQLEVHIGWLLLQAPRWVFKEEDP 123

Qy        128 LFLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYES 187
              : |||| |:|  ::|| | ::|:  ||:: | :  |  ||::|||:|:| | |   :  |
Db        124 IHLRCHSWKNTALHKVTYLQNGKDRKYFHHNSDFHIPKATLKDSGSYFCRGLVGSKNVSS 183

Qy        188 EPLNITVIKAPREKYWLQFFIP-------LLVVILFAVDTGLFISTQQQV 230
              | :|||: :          |  |       |:|:|||||||: | :  :
Db        184 ETVNITITQGLAVSTISSFSPPGYQVSFCLVMVLLFAVDTGLYFSVKTNI 233


RESULT 9
Q8R477
ID   Q8R477      PRELIMINARY;      PRT;   249 AA.
AC   Q8R477;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Transmembrane receptor CD16-2.
GN   FCRL3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL; TISSUE=Liver;
RA   Mechetina L.V., Najakshin A.M., Alabyev B.Y., Chikaev N.A.,
RA   Taranin A.V.;
RT   "Identification of CD16-2, a novel mouse receptor homologous to
RT   CD16/FcgRIII.";
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF499613; AAM19249.1; -.
DR   MGD; MGI:2179523; Fcrl3.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Receptor.
SQ   SEQUENCE   249 AA;  28382 MW;  3DEAF3D935BEF5CD CRC64;

  Query Match             28.9%;  Score 401.5;  DB 11;  Length 249;
  Best Local Similarity   38.9%;  Pred. No. 3.9e-28;
  Matches   88;  Conservative   40;  Mismatches   87;  Indels   11;  Gaps    2;

Qy         10 LLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGS 69
              ||  ||:  |  |: |  ||  |:|:| | |: : ::||| | |    | :| |||| |
Db          5 LLPTALVLTAFSGIQAGLQKAVVNLDPKWVRVLEEDSVTLRCQGTFSPEDNSIKWFHNES 64

Qy         70 LSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLF 129
              |    :::  | :|: :||| |:||       |:|| |||   |||||  :  :  || |:
Db         65 LIPHQDANYVIQSARVKDSGMYRCQTALSTISDPVQLEVHMGWLLLQTTKWLFQEGDPIH 124

Qy        130 LRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEP 189
              |||| |:|  | || | ::|:  ||::||  :  |  ||  |||:|:|  | :   :  |
Db        125 LRCHSWQNRPVRKVTYLQNGKGKKYFHENSELPIPKATHNDSGSYFCRGLIGHNNKSSAS 184
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Qy        190 LNITV-------IKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQ 228
                |::       :  |    | |    ||: :|||:|| |: | ::
Db        185 FRISLGDPGSPSMFPP----WHQITFCLLIGLLFAIDTVLYFSVRR 226


RESULT 10
Q8R2R4
ID   Q8R2R4      PRELIMINARY;      PRT;   249 AA.
AC   Q8R2R4;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
GN   FCRL3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC027310; AAH27310.1; -.
DR   MGD; MGI:2179523; Fcrl3.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Hypothetical protein.
SQ   SEQUENCE   249 AA;  28372 MW;  740D6BE8E1536224 CRC64;

  Query Match             28.7%;  Score 399.5;  DB 11;  Length 249;
  Best Local Similarity   38.9%;  Pred. No. 5.9e-28;
  Matches   88;  Conservative   40;  Mismatches   87;  Indels   11;  Gaps    2;

Qy         10 LLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGS 69
              ||  ||:  |  |: |  ||  |:|:| | |: : ::||| | |     | :| |||||
Db          5 LLPTALVLTAFSGIQAGLQKAVVNLDPKWVRVLEEDSVTLRCQGTFSPEDNSIKWFHNES 64

Qy         70 LSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLF 129
              |    :::  | :|: :||| |:||      |:|| |||   ||||| :  :  || |:
Db         65 LIPHQDANYVIQSARVKDSGMYRCQTALSTISDPVQLEVHMGWLLLQTTKWLFQEGDPIH 124

Qy        130 LRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEP 189
              |||| |:|  | || | ::|:  ||::||  :  |  ||  |||:|:| | :   :  |
Db        125 LRCHSWQNRPVRKVTYSQNGKGKKYFHENSELLIPKATHNDSGSYFCRGLIGHNNKSSAS 184

Qy        190 LNITV-------IKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQ 228
                |::       :  |    | |    ||: :|||:|| |: | ::
Db        185 FRISLGDPGSPSMFPP----WHQITFCLLIGLLFAIDTVLYFSVRR 226


RESULT 11
Q9ES92
ID   Q9ES92      PRELIMINARY;      PRT;   261 AA.
AC   Q9ES92;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fc gamma receptor III.
GN   FCGR3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Fossati Jimack L., Boucrot E., Izui S.;
RT   "Mouse Fc gamma RIII: identification and characterization of a new
RT   allele in C57BL/6 mice.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Ovary, and Uterus;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AF197930; AAG28520.1; -.
DR   EMBL; AK077227; BAC36696.1; -.
DR   MGD; MGI:95500; Fcgr3.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Receptor.
SQ   SEQUENCE   261 AA;  30098 MW;  9C8570E032F94730 CRC64;

  Query Match             28.6%;  Score 398;  DB 11;  Length 261;
  Best Local Similarity   37.8%;  Pred. No. 8.5e-28;
  Matches   85;  Conservative   39;  Mismatches   95;  Indels    6;  Gaps    3;

Qy         11 LCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHN-GS 69
              | : |||    |    |    |  | |:||| :: | : ||| | | :    |||:|||| |
Db         16 LTILLLFAFADRQSAALPKAVVKLDPPWIQVLKEDMVTLMCEGTHNPGNSSTQWFHNWSS 75

Qy         70 LSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLF 129
              :  :  ||      |   |||||:|| :|   |:|| | | |||||||    | :||: :
Db         76 IRSQVQSSYTF-KATVNDSGEYRCQMEQTRLSDPVDLGVISDWLLLQTPQRVFLEGETIT 134

Qy        130 LRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEP 189
              |||| |||  : :: :: : ::::| :   | ||  |    || ||| | :    ::|:|
Db        135 LRCHSWRNKLLNRISFFHNEKSVRYHHYKSNFSIPKANHSHSGDYYCKGSLGSTQHQSKP 194

Qy        190 LNITV----IKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQV 230
              : |||      :      |      |:: :|||||||:   :: :
Db        195 VTITVQDPATTSSISLVWYHTAFSLVMCLLFAVDTGLYFYVRRNL 239


RESULT 12
Q7TMW9
ID   Q7TMW9      PRELIMINARY;      PRT;   261 AA.
AC   Q7TMW9;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Similar to Fc gamma receptor.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA   Strausberg R.;
RL   Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC052819; AAH52819.1; -.
KW   Receptor.
SQ   SEQUENCE   261 AA;  30032 MW;  81389D45C2E14730 CRC64;

  Query Match             27.8%;  Score 386;  DB 11;  Length 261;
  Best Local Similarity   37.3%;  Pred. No. 1e-26;
  Matches   84;  Conservative   39;  Mismatches   96;  Indels    6;  Gaps    3;

Qy         11 LCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHN-GS 69
              | : |||    |   |    |  | |:||| :: | : ||| | | :     |||:|||| |
Db         16 LTILLLFAFADRQSAALPKAVVKLDPPWIQVLKEDMVTLMCEGTHNPGNSSTQWFHNWSS 75

Qy         70 LSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLF 129
              :  :  ||      |   |||||:|| :|   |:|| | | |||||||     | :||: :
Db         76 IRSQVQSSYTF-KATVNDSGEYRCQMEQTRLSDPVDLGVISDWLLLQTPQRVFLEGETIT 134

Qy        130 LRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEP 189
              |||  |||  : :: :: : ::::| :   | ||  |    || ||| | :    ::|:|
Db        135 LRCPSWRNKLLNRISFFHNEKSVRYHHYKSNFSIPKANHSHSGDYYCKGSLGSTQHQSKP 194

Qy        190 LNITV----IKAPREKYWLQFFIPLLVVILFAVDTGLFISTQQQV 230
              : |||      :     |       |:: :||||||||:   :: :
Db        195 VTITVQDPATTSSISLVWHHTAFSLVMCLLFAVDTGLYFYVRRNL 239


RESULT 13
Q8SPW5
ID   Q8SPW5      PRELIMINARY;      PRT;   357 AA.
AC   Q8SPW5;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fc gamma receptor I.
GN   FCGR1.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Namenuk A.K., Hong K., Meng Y.G., Shields R.L., Cromwell M.E.M.,
RA   Presta L.G.;
RT   "Binding of human IgG to cynomolgus FcR.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF485812; AAL92095.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00409; IG; 3.
DR   PROSITE; PS50835; IG_LIKE; 3.
KW   Receptor.
SQ   SEQUENCE   357 AA;  40715 MW;  F5C51A06A3BCB08F CRC64;

  Query Match             27.6%;  Score 383.5;  DB 6;  Length 357;
  Best Local Similarity   40.7%;  Pred. No. 2.6e-26;
  Matches   74;  Conservative   38;  Mismatches   67;  Indels    3;  Gaps    3;

Qy         14 ALLFFAP-DGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSE 72
              ||| : | || :    |  ::| |||  :|: | ||| |         |||:|| ||: ::
Db          6 ALLLWVPVDGQVDT-TKAVITLQPPWVSVFQEETVTLQCEVPRLPGSSSTQWFLNGTATQ 64

Qy         73 ETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRC 132
                :  |  | :|  :|||||:||      |:|: ||:  |||||| |: |  ||:|| |||
Db         65 TSTPSYRITSASVKDSGEYRCQRGPSGRSDPIQLEIHRDWLLLQVSSRVFTEGEPLALRC 124

Qy        133 HGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNI 192
              | |::  || |:||::|:| |::| |  ::|    :  :| |:|:| : :  | |  :::
Db        125 HAWKDKLVYNVLYYQNGKAFKFFYRNSQLTILKTNISHNGAYHCSG-MGKHRYTSAGVSV 183

Qy        193 TV 194
              ||
Db        184 TV 185


RESULT 14
Q8SPW3
ID   Q8SPW3      PRELIMINARY;      PRT;   294 AA.
AC   Q8SPW3;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fc gamma receptor IIb.
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Namenuk A.K., Hong K., Meng Y.G., Shields R.L., Cromwell M.E.M.,
RA   Presta L.G.;
RT   "Binding of human IgG to cynomolgus FcR.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF485814; AAL92097.1; -.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR007110; Ig-like.
DR   Pfam; PF00047; ig; 2.
DR   SMART; SM00409; IG; 2.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Receptor.
SQ   SEQUENCE   294 AA;  32151 MW;  A8D476A448E3D01E CRC64;

  Query Match             27.4%;  Score 380.5;  DB 6;  Length 294;
  Best Local Similarity   35.0%;  Pred. No. 3.8e-26;
  Matches   86;  Conservative   42;  Mismatches   99;  Indels   19;  Gaps    4;

Qy         10 LLCVALLFFAP-DGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNG 68
              ||  |:|| ||  |  | | |  : | |||  : : ::|||| | :  :  ||:|||||
Db         29 LLWTAVLFLAPVAGTPAAPPKAVLKLEPPWINVLREDSVTLTCGGAHSPDSDSTQWFHNG 88

Qy         69 SLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPL 128
              :|            |   |||||:||  : : |:||:| | |:|| ||        ||: :
Db         89 NLIPTHTQPSYRFKANNNDSGEYRCQTGRTSLSDPVHLTVLSEWLALQTPHLEFREGETI 148

Qy        129 FLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESE 188
              ||||  |::  : || ::::| : |: : | | ||  |     || |:||| :    | |:
Db        149 LLRCHSWKDKPLIKVTFFQNGISKKFSHMNPNFSIPQANHSHSGDYHCTGNIGYTPYSSK 208

Qy        189 PLNITVIKAPREKYWLQFFIPLL-----VVILFAVDTGLFIST-QQQVTFLLKIKRTRKG 242
              |: |||              :| :     : |: || ||: ::     |  |:  :: |
Db        209 PVTITV------------QVPSMGSSSPIGIIVAVVTGIAVAAIVAAVVALIYCRKKRIS 256

Qy        243 FRLLNP 248
                 ||
Db        257 ANPTNP 262


RESULT 15
Q8R142
ID   Q8R142      PRELIMINARY;      PRT;   330 AA.
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AC   Q8R142;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC025535; AAH25535.1; -.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 3.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS50835; IG_LIKE; 2.
KW   Hypothetical protein; Immunoglobulin domain.
FT   NON_TER       1       1
SQ   SEQUENCE   330 AA;  37116 MW;  891F8724F870D8BE CRC64;

  Query Match             27.3%;  Score 379;  DB 11;  Length 330;
  Best Local Similarity   37.8%;  Pred. No. 6e-26;
  Matches   90;  Conservative   42;  Mismatches   94;  Indels   12;  Gaps    6;

Qy          10 LLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGS 69
               ||   ||:    | :    |  ::| |||  ||: ||||| | | :    |||:|| ||:
Db           6 LLTTLLLWVPVGGEVVNATKAVITLQPPWASIFQKENVTLWCEGPHLPGDSSTQWFINGT 65

Qy          70 LSEETNSSLNIVNAKFEDSGEYKCQHQQVNESEPVYLEVF-SDWLLLQASAEVVMEGQPL 128
               : : :  | :|  | |:|||||:||       |:|| |::   |||||||  |: ||:||
Db          66 VVQTSTPSYSISVASFQDSGEYRCQIGSSVPSDPVQLQIHKEDWLLLQASRRVLTEGEPL 125

Qy         129 FLRCHGWRNWDVYKVIYYKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESE 188
               ||||||:|  || |::|::|:: |:       |:|    :  || |:|:| : :  | |
Db         126 ALRCHGWKNKLVYNVVFYRNGKSFKF-SSGSKIAILKTNLSHSGIYHCSG-MGRHRYTSA 183

Qy         189 PLNITVIKAPREKYWLQFFIPLL-VVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRL 245
               ::|||   | |     |  |:|   :      |  ::   :   ||:    | | :|
Db         184 GVSITVKAFPLE----LFTTPVLRASVSSPFPEGSLVTLNCETNLLLQ----RPGLQL 233


Search completed: October  6, 2004, 09:07:01
Job time : 44.4371 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:14:29 ; Search time 3370.32 Seconds
(without alignments)
9953.801 Million cell updates/sec

Title: US-10-763-400-4
Perfect score: 774
Sequence: 1 atggctcctgccatggaatc.....caaaccccaaaaacaactga 774

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
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13: gb_un:*
14: gb_vi:*
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16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
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36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		774	100.0	774	6	AR175481	AR175481 Sequence
2	c	774	100.0	774	6	AR175482	AR175482 Sequence
3		774	100.0	1068	6	A21606	A21606 human FC ep
4		774	100.0	1068	6	BD264325	BD264325 Recombina
5		774	100.0	1068	6	AX026808	AX026808 Sequence
6		774	100.0	1081	9	HUMMCIAA	J03605 Human mast
7		774	100.0	1102	9	BC005912	BC005912 Homo sapi
8		774	100.0	1174	6	AR123794	AR123794 Sequence
9		774	100.0	1198	6	AR175479	AR175479 Sequence
10	c	774	100.0	1198	6	AR175480	AR175480 Sequence
11		774	100.0	1198	6	AX074287	AX074287 Sequence
12	c	774	100.0	1198	6	AX074289	AX074289 Sequence
13		774	100.0	1198	6	AX101304	AX101304 Sequence
14		774	100.0	1198	6	AX335621	AX335621 Sequence
15		774	100.0	1198	9	HSFCERI	X06948 Human mRNA
16		773	99.9	773	6	AR219964	AR219964 Sequence
17		772.4	99.8	1106	9	BC015195	BC015195 Homo sapi
18		766	99.0	1198	6	I09686	I09686 Sequence 3
19		699	90.3	699	6	AR175483	AR175483 Sequence
20		696	89.9	696	6	AX074290	AX074290 Sequence
21	c	696	89.9	696	6	AX074292	AX074292 Sequence
22		611	78.9	2955	6	AR219962	AR219962 Sequence
23		591	76.4	591	6	AR175486	AR175486 Sequence
24		591	76.4	591	6	AX074293	AX074293 Sequence
25	c	591	76.4	591	6	AX074295	AX074295 Sequence
26		591	76.4	713	6	E07699	E07699 cDNA encodi
27		591	76.4	1983	6	AX074312	AX074312 Sequence
28	c	591	76.4	1983	6	AX074314	AX074314 Sequence
29		591	76.4	2268	6	AX074303	AX074303 Sequence
30	c	591	76.4	2268	6	AX074305	AX074305 Sequence
31		547.4	70.7	560	6	BD264322	BD264322 Recombina
32		547.4	70.7	560	6	AX026805	AX026805 Sequence
33		528	68.2	528	6	AX274969	AX274969 Sequence
34		516.4	66.7	528	6	BD267591	BD267591 Crystalli
35		516	66.7	516	6	AR175487	AR175487 Sequence
36		516	66.7	516	6	AX074296	AX074296 Sequence
37	c	516	66.7	516	6	AX074298	AX074298 Sequence
38		516	66.7	1908	6	AX074315	AX074315 Sequence
39	c	516	66.7	1908	6	AX074317	AX074317 Sequence
40		516	66.7	2193	6	AX074306	AX074306 Sequence
41	c	516	66.7	2193	6	AX074308	AX074308 Sequence
42		515.2	66.6	528	6	AX274971	AX274971 Sequence
43		508	65.6	516	6	BD267592	BD267592 Crystalli
44		440.4	56.9	1082	4	OAR18205	Y18205 Ovis aries
45		438.4	56.6	984	4	ECA18204	Y18204 Equus cabal

ALIGNMENTS

RESULT 1
AR175481
LOCUS AR175481 774 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 4 from patent US 6309832.
ACCESSION AR175481
VERSION AR175481.1 GI:17916780
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 774)
AUTHORS Frank,G.R., Porter,J.P., Rushlow,K.E. and Wassom,D.L.
TITLE Method to detect IgE
JOURNAL Patent: US 6309832-A 4 30-OCT-2001;
FEATURES Location/Qualifiers

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                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 774;  DB 6;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 9.5e-225;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
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Db        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
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Db        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774


RESULT 2
AR175482/c
LOCUS       AR175482                774 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 5 from patent US 6309832.
ACCESSION   AR175482
VERSION     AR175482.1  GI:17916781
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 774)
  AUTHORS   Frank,G.R., Porter,J.P., Rushlow,K.E. and Wassom,D.L.
  TITLE     Method to detect IgE
  JOURNAL   Patent: US 6309832-A 5 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .774
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 774;  DB 6;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 9.5e-225;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 715

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
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Db        714 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 655

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Db        654 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 595

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
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Db        594 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 535

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 475

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 415

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
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Db        414 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 355

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
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Db        354 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 295

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
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Db        294 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 235

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 175

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 115

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 55

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         54 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 1


RESULT 3
A21606
LOCUS       A21606                  1068 bp    DNA     linear   PAT 21-JUL-1994
DEFINITION  human FC epsilon RIIa.
ACCESSION   A21606
VERSION     A21606.1  GI:579605
KEYWORDS    .
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1068)
  AUTHORS   .
  TITLE     HYBRID Fc RECEPTOR MOLECULES
  JOURNAL   Patent: WO 9106570-A 29 16-MAY-1991;
FEATURES             Location/Qualifiers
     source          1. .1068
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     gene            40. .813
                     /gene="FC epsilon RIIa"
     CDS             40. .813
                     /gene="FC epsilon RIIa"
                     /codon_start=1
                     /protein_id="CAA01564.1"
                     /db_xref="GI:579606"
                     /db_xref="GOA:P12319"
                     /db_xref="SWISS-PROT:P12319"
                     /translation="MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKG
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                     PVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHN
                     ISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAV
                     DTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN"
ORIGIN

  Query Match            100.0%;  Score 774;  DB 6;  Length 1068;
  Best Local Similarity  100.0%;  Pred. No. 1e-224;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 99

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 159

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Db        160 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 219

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 279

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 339

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 399

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
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Db        400 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 459

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 519

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 579

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
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Db        580 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 639

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 699

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
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Db        700 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 759

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
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Db        760 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 813
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RESULT 4
BD264325
LOCUS       BD264325                1068 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Recombinant soluble Fc receptors.
ACCESSION   BD264325
VERSION     BD264325.1  GI:33074093
KEYWORDS    JP 2002531086-A/8.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1068)
  AUTHORS   Sondermann,P., Huber,R. and Jakob,U.
  TITLE     Recombinant soluble Fc receptors
  JOURNAL   Patent: JP 2002531086-A 8 24-SEP-2002;
            MAX PLANCK GESELLSCHAFT ZUR FOERDERUNG DER WISSENSCHAFTEN EV
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002531086-A/8
            PD   24-SEP-2002
            PF   03-DEC-1999 JP 2000585398
            PR   03-DEC-1998 EP   98122969.3
            PI   PETER SONDERMANN,ROBERT HUBER,UWE JAKOB
            PC   C12N15/09,A61K38/00,A61K45/00,A61P19/02,A61P29/00,A61P31/18,
            PC   A61P35/00,
            PC   A61P37/02,A61P37/08,C07K14/735,C12N1/21,G01N33/53,G01N33/53//
            PC   (C12N1/21,C12R1:19),C12N15/00,A61K37/02
            CC   Description of Artificial Sequence: Primer
            FH   Key             Location/Qualifiers
            FT   source          1. .1068
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .1068
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                     /db_xref="taxon:9606"
ORIGIN

  Query Match            100.0%;  Score 774;  DB 6;  Length 1068;
  Best Local Similarity  100.0%;  Pred. No. 1e-224;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 99

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 159

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 219

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 279

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 339
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Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 399

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 459

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 519

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
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Db        520 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 579

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
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Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 699

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 759

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 813
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RESULT 5
AX026808
LOCUS AX026808 1068 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 14 from Patent EP1006183.
ACCESSION AX026808
VERSION AX026808.1 GI:10187941
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS .
TITLE Recombinant soluble fc receptors
JOURNAL Patent: EP 1006183-A 14 07-JUN-2000;
MAX PLANCK GESELLSCHAFT (DE)
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 774; DB 6; Length 1068;
Best Local Similarity 100.0%; Pred. No. 1e-224;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
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Db         40 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 99

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 159

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 279

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 339

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 399

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 459

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 519

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
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Db        520 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 579

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
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Db        580 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 639

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
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Db        640 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 699

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
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Db        700 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 759

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
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Db        760 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 813
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RESULT 6
HUMMCIAA
LOCUS HUMMCIAA 1081 bp mRNA linear PRI 11-JUN-1993
DEFINITION Human mast cell IgE receptor alpha-chain.
ACCESSION J03605
VERSION J03605.1 GI:187449
KEYWORDS immunoglobulin-like sequence; receptor.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1081)
AUTHORS Shimizu,A., Tepler,I., Benfey,P.N., Berenstein,E.H.,
Siraganian,R.P. and Leder,P.
TITLE Human and rat mast cell high-affinity immunoglobulin E receptors:
characterization of putative alpha-chain gene products
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (6), 1907-1911 (1988)
MEDLINE 88158102
PUBMED 2964640
COMMENT Original source text: Human mast cell line KU812, cDNA to mRNA,
clone pAS-h-IgER-110B.
Computer-readable copy of sequence in [1] kindly provided by
P.Leder, 08-FEB-1988.
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/mol_type="mRNA"
/db_xref="taxon:9606"
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/product="mast cell IgE receptor alpha-chain mRNA"
CDS 35. .808
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                     ISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAV
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ORIGIN      Unreported.

  Query Match           100.0%;  Score 774;  DB 9;  Length 1081;
  Best Local Similarity  100.0%;  Pred. No. 1e-224;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
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Db         35 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 94

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
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Db         95 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 154

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Db        155 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 214

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
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Db        215 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 274

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
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Db        275 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 334

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
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Db        335 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 394

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
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Db        395 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 454

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
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Db        455 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 514

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
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Db        515 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 574

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
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Db        575 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 634

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
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Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
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Db        695 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 754

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
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Db        755 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 808


RESULT 7
BC005912
LOCUS       BC005912               1102 bp    mRNA    linear   PRI 03-OCT-2003
DEFINITION  Homo sapiens Fc fragment of IgE, high affinity I, receptor for;
            alpha polypeptide, mRNA (cDNA clone MGC:14507 IMAGE:4294467),
            complete cds.
ACCESSION   BC005912
VERSION     BC005912.1  GI:13543505
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1102)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1102)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-APR-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 21 Row: h Column: 16
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4503674.
FEATURES             Location/Qualifiers
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                     /tissue_type="Prostate"
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                     /note="synonyms: FCE1A, FcERI"
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                     ISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAV
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  Best Local Similarity   100.0%;  Pred. No. 1e-224;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         30 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 89

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
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Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
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Db        210 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 269

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
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Db        270 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 329

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
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Db        330 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 389

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
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Db        390 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 449

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
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Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
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Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
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Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
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Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
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Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
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RESULT 8
AR123794
LOCUS       AR123794                1174 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 10 from patent US 6171803.
ACCESSION   AR123794
VERSION     AR123794.1  GI:14109155
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1174)
  AUTHORS   Kinet,J.Pierre.
  TITLE     Isolation, characterization, and use of the human .beta. subunit of
            the high affinity receptor for immunoglobulin E
  JOURNAL   Patent: US 6171803-A 10 09-JAN-2001;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             100.0%;  Score 774;  DB 6;  Length 1174;
  Best Local Similarity   100.0%;  Pred. No. 1e-224;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
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Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
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Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
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Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
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Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
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Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
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Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
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RESULT 9
AR175479
LOCUS       AR175479                1198 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 1 from patent US 6309832.
ACCESSION   AR175479
VERSION     AR175479.1  GI:17916778
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1198)
  AUTHORS   Frank,G.R., Porter,J.P., Rushlow,K.E. and Wassom,D.L.
  TITLE     Method to detect IgE
  JOURNAL   Patent: US 6309832-A 1 30-OCT-2001;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             100.0%;  Score 774;  DB 6;  Length 1198;
  Best Local Similarity   100.0%;  Pred. No. 1e-224;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
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Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
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Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
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Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880


RESULT 10
AR175480/c
LOCUS       AR175480                1198 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 3 from patent US 6309832.
ACCESSION   AR175480
VERSION     AR175480.1  GI:17916779
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1198)
  AUTHORS   Frank,G.R., Porter,J.P., Rushlow,K.E. and Wassom,D.L.
  TITLE     Method to detect IgE
  JOURNAL   Patent: US 6309832-A 3 30-OCT-2001;
FEATURES             Location/Qualifiers
     source          1. .1198
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 774;  DB 6;  Length 1198;
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  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1092 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 1033

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 973

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
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Db        912 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 853

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
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Db        852 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 793

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        792 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 733

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        732 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 673

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        672 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 613

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 553

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
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Db        552 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 493

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 433

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 373

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 319


RESULT 11
AX074287
LOCUS       AX074287               1198 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 1 from Patent WO0104310.
ACCESSION   AX074287
VERSION     AX074287.1  GI:12710474
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Weber,E.R., Wood,K.V. and Hall,M.P.
  TITLE     Fc epsilon receptor-luminescence inducing protein chimeric nucleic
            acid molecules, fusion proteins and uses thereof
  JOURNAL   Patent: WO 0104310-A 1 18-JAN-2001;
            Heska Corporation (US) ; PROMEGA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .1198
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             107. .880
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC28463.1"
                     /db_xref="GI:12710475"
                     /db_xref="REMTREMBL:CAC28463"
                     /translation="MAPAMESPTLLCVALLFFAPDGVLAVPQKPKVSLNPPWNRIFKG
                     ENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKFEDSGEYKCQHQQVNESE
                     PVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIYYKDGEALKYWYENHN
                     ISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQFFIPLLVVILFAV
                     DTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN"
ORIGIN

  Query Match           100.0%;  Score 774;  DB 6;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 1e-224;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880


RESULT 12
AX074289/c
LOCUS       AX074289               1198 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 3 from Patent WO0104310.
ACCESSION   AX074289
VERSION     AX074289.1  GI:12710476
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Weber,E.R., Wood,K.V. and Hall,M.P.
  TITLE     Fc epsilon receptor-luminescence inducing protein chimeric nucleic
            acid molecules, fusion proteins and uses thereof
  JOURNAL   Patent: WO 0104310-A 3 18-JAN-2001;
            Heska Corporation (US) ; PROMEGA CORPORATION (US)
FEATURES             Location/Qualifiers
     source          1. .1198
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 774;  DB 6;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 1e-224;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
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Db       1092 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 1033

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 973

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 913
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Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        912 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 853

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        852 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 793

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        792 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 733

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        732 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 673

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        672 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 613

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 553

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 493

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
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Db        492 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 433

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 373

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
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Db        372 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 319
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RESULT 13
AX101304
LOCUS AX101304 1198 bp DNA linear PAT 10-APR-2001
DEFINITION Sequence 7 from Patent WO0121816.
ACCESSION AX101304
VERSION AX101304.1 GI:13620094
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kinet,J.P., Donnadieu,E., Jouvin,M.H., Cookson,W. and Moffatt,M.F.
TITLE Modulation of ige receptor cell surface expression
JOURNAL Patent: WO 0121816-A 7 29-MAR-2001;
ISIS INNOVATION LIMITED (GB) ; Beth Israel Deaconess Medical Center, Inc. (US)
FEATURES Location/Qualifiers
source 1. .1198
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 774; DB 6; Length 1198;
Best Local Similarity 100.0%; Pred. No. 1e-224;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
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Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166
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Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
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Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
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Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
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Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
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RESULT 14
AX335621
LOCUS AX335621 1198 bp DNA linear PAT 09-JAN-2002
DEFINITION Sequence 6130 from Patent WO0194629.
ACCESSION AX335621
VERSION AX335621.1 GI:18126340
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G., Horrigan,S., Soppet,D.R. and Weaver,Z.
TITLE Cancer gene determination and therapeutic screening using signature gene sets
JOURNAL Patent: WO 0194629-A 6130 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES Location/Qualifiers
source 1. .1198
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 1e-224;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
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Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
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Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
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Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
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Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
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Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
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RESULT 15
HSFCERI
LOCUS       HSFCERI                 1198 bp    mRNA    linear   PRI 21-MAR-1995
DEFINITION  Human mRNA for high affinity IgE receptor alpha-subunit (FcERI).
ACCESSION   X06948
VERSION     X06948.1  GI:31317
KEYWORDS    FcERI gene; IgE receptor alpha-subunit.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1198)
  AUTHORS   Kochan,J., Pettine,L.F., Hakimi,J., Kishi,K. and Kinet,J.P.
  TITLE     Isolation of the gene coding for the alpha subunit of the human
            high affinity IgE receptor
  JOURNAL   Nucleic Acids Res. 16 (8), 3584 (1988)
  MEDLINE   88233953
   PUBMED   2967464
REFERENCE   2  (bases 1 to 1198)
  AUTHORS   Kochan,J.P.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-FEB-1988) Kochan J. P., Hoffman-La Roche, Dept
            Molecular Genetics, 340 Kingsland, Nutley, New Jersey 07110
COMMENT     *source cell line=KU812; library=lambda gt11 cDNA.
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                     /mol_type="mRNA"
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                     /product="mature IgE receptor (AA 1-232)"
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     misc_feature    719. .778
                     /note="put. transmembrane region"
     misc_feature    779. .877
                     /note="put. cytoplasmic tail"
ORIGIN

  Query Match           100.0%;  Score 774;  DB 9;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 1e-224;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
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Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
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Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
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Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
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Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
```

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Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
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Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
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Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
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Job time : 3370.32 secs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 8, 2004, 15:03:47 ; Search time 376.347 Seconds
(without alignments)
8736.904 Million cell updates/sec

Title: US-10-763-400-4
Perfect score: 774
Sequence: 1 atggctcctgccatggaatc.....caaaccccaaaaacaactga 774

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: geneseqn2002s:*
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8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	774	100.0	774	4	AAF97964	Aaf97964 Human imm
2	774	100.0	1068	3	AAA27470	Aaa27470 Human Fc
3	774	100.0	1088	1	AAN90126	Aan90126 cDNA enco
4	774	100.0	1174	2	AAQ51020	Aaq51020 Human Fce
5	774	100.0	1197	2	AAT85615	Aat85615 Alpha sub
6	774	100.0	1198	2	AAV36343	Aav36343 cDNA enco
7	774	100.0	1198	3	AAA34813	Aaa34813 Human ade
8	774	100.0	1198	3	AAF20935	Aaf20935 Human hig
9	774	100.0	1198	4	AAF77692	Aaf77692 Human wil
c 10	774	100.0	1198	5	AAF24912	Aaf24912 Complemen
11	774	100.0	1198	5	AAF24911	Aaf24911 Nucleotid
12	774	100.0	1198	6	ABL67793	Oesophagu
13	774	100.0	1198	7	ABZ96629	Abz96629 Human hig
14	774	100.0	1198	9	ADB85535	Adb85535 Human imm
15	774	100.0	21742	3	AAA34816	Aaa34816 Human ade
16	774	100.0	21742	3	AAF20938	Aaf20938 Human hig
17	774	100.0	21742	7	ABZ96632	Abz96632 Human hig
18	774	100.0	117608	7	ABZ97129	Abz97129 Human rec
19	774	100.0	117609	3	AAF21435	Aaf21435 Human rec
20	773	99.9	773	6	ABS52959	Abs52959 Human cDN
21	772.4	99.8	898	8	ACD06182	Acd06182 Human cDN
22	771.4	99.7	773	2	AAV20402	Aav20402 Human IgE
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24	769.2	99.4	1193	2	AAQ04644	Aaq04644 Encodes a
c 25	696	89.9	696	5	AAF24914	Aaf24914 Complemen
26	696	89.9	696	5	AAF24913	Aaf24913 Nucleotid
27	611	78.9	2955	2	AAV20404	Aav20404 Plasmid R
28	611	78.9	2955	6	ABS52957	Abs52957 Human cDN
29	599.8	77.5	1150	2	AAQ34840	Aaq34840 Human hig
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c 31	591	76.4	591	5	AAF24916	Aaf24916 Complemen
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33	591	76.4	713	2	AAQ55969	Aaq55969 Human dih
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c 36	591	76.4	2268	5	AAF24921	Aaf24921 Complemen
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38	554	71.6	570	3	AAA27472	Aaa27472 Recombina
39	530	68.5	757	8	ACD06183	Acd06183 Human cDN
40	528	68.2	528	3	AAA27301	Aaa27301 Human Fce
41	528	68.2	528	4	AAH47768	Aah47768 Nucleotid
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43	516	66.7	516	5	AAF24917	Aaf24917 DNA encod
c 44	516	66.7	516	5	AAF24918	Aaf24918 Complemen
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ALIGNMENTS

RESULT 1
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ID AAF97964 standard; cDNA; 774 BP.
XX
AC AAF97964;
XX
DT 19-JUN-2001 (first entry)
XX
DE Human immunoglobulin E receptor I alpha subunit coding sequence.
XX
KW Human; polymorphism; immunoglobulin E receptor I alpha subunit; IGERA;
KW single nucleotide polymorphism; SNP; allele specific oligonucleotide;
KW immunoassay; detection; ss.
XX
OS Homo sapiens.
XX
PN WO200111010-A2.
XX
PD 15-FEB-2001.
XX
PF 02-AUG-2000; 2000WO-US021097.
XX
PR 09-AUG-1999; 99US-0147860P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Denton RR, Duda A, Kliem SE, Lanz EM, Nandabalan K;
PI Stephens JC;
XX
DR WPI; 2001-202766/20.
DR P-PSDB; AAB74667.
XX
PT New polynucleotide for gene therapy, comprises nucleotide polymorphisms
PT in the immunoglobulin E receptor I alpha subunit gene.
XX
PS Claim 7; Fig 2; 99pp; English.
XX
CC The present invention describes an isolated polynucleotide (I) comprising
CC a nucleotide sequence (S) which is a polymorphic variant of a reference
CC sequence for the human immunoglobulin E receptor I alpha subunit (IGERA)
CC gene or its fragment. The polymorphic variant comprises at least one
CC polymorphism selected from guanine (G) at polymorphic site (PS) 1, PS9,
CC PS10 or PS21, cytosine (C) at PS2, PS3, PS6, PS12, PS18 or PS20, adenine
CC (A) at PS5, PS7, PS11, PS13, PS14, PS15, PS19, or PS22 and thymine (T) at
CC PS4, PS8, PS16 or PS17, or (G) at a position corresponding to nucleotide
CC 251, (A) at a position corresponding to nucleotide 302 or 741, and (T) at

CC a position corresponding to nucleotide 530. (I) can be used in gene
CC therapy. (I) is useful for therapeutic purposes. A polypeptide (II)
CC encoded by (I) is useful in drug screening assays and in assays to
CC measure the binding affinity of one or more candidate drugs targeting
CC (II). An antibody (III) to (II) is useful to immunoprecipitate (II) from
CC solution and also reacts with (II) on Western or immunoblots of
CC polyacrylamide gels on membrane supports or substrates. (III) is also
CC useful in immunoassays to detect (II) in biological samples. AAF97965 to
CC AAF98096 represent IGERA allele specific oligonucleotide probes; AAF98097
CC to AAF98140 represent IGERA gene polymorphism detection primers; and
CC AAF98141 to AAF98180 represent IGERA gene PCR primers which are used in
CC the exemplification of the present invention. The present sequence
CC encodes the human IGERA protein used in the present invention
XX
SQ Sequence 774 BP; 221 A; 172 C; 177 G; 204 T; 0 U; 0 Other;

Query Match 100.0%; Score 774; DB 4; Length 774;
Best Local Similarity 100.0%; Pred. No. 2.4e-223;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
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Db          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
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Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
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Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
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Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
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Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
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Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
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Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
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Db        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
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RESULT 2
AAA27470
ID AAA27470 standard; cDNA; 1068 BP.
XX
AC AAA27470;
XX
DT 11-SEP-2000 (first entry)
XX
DE Human Fc receptor, FcepsilonRIa, coding sequence.
XX
KW Human; Fc receptor; FcepsilonRIa; immunoglobulin; infection;
KW immune response; HIV; IgG; immunosuppressive; antirheumatic;
KW antiinflammatory; AIDS; SLE; multiple myeloma; rheumatoid arthritis;
KW systemic lupus erythematosus; tumour; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 31. .813
FT /*tag= a
FT /product= "FcepsilonRIa"
XX
PN EP1006183-A1.
XX
PD 07-JUN-2000.
XX
PF 03-DEC-1998; 98EP-00122969.
XX
PR 03-DEC-1998; 98EP-00122969.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
DR WPI; 2000-367968/32.
DR P-PSDB; AAY96230.
XX
PT Novel Fc receptor lacking transmembrane domains, a signal peptide, and
PT glycosylation, useful for diagnosing and treating immune disorders and
PT cancer.
XX
PS Disclosure; Page 17; 60pp; English.
XX
CC The present sequence is the human Fc receptor, FcepsilonRIa, coding
CC sequence. Fc receptors play a key role in defending the body against
CC infections. First, pathogens are opsonised by serum immunoglobulins. The
CC resulting complex then binds to cells expressing Fc receptors. Upon Fc
CC receptor activation, immune effector pathways are activated, leading to
CC immune response. The present sequence may be modified to produce
CC recombinant versions. The recombinant Fc receptor consist only of the
CC extracellular portion of the receptor and are not glycosylated i.e. they
CC do not have transmembrane domains or signal peptides. The recombinant
CC proteins may be used in immunoassays to determine the immune status of
CC patients with chronic diseases of the immune system, e.g. AIDS, systemic
CC lupus erythematosus (SLE), multiple myeloma (MM), or rheumatoid
CC arthritis. In addition, pharmaceutical compositions containing
CC recombinant proteins may be used to treat or prevent autoimmune diseases,
CC allergies or tumours, especially AIDS, rheumatoid arthritis or MM
XX
SQ Sequence 1068 BP; 330 A; 215 C; 229 G; 294 T; 0 U; 0 Other;

Query Match 100.0%; Score 774; DB 3; Length 1068;
Best Local Similarity 100.0%; Pred. No. 2.8e-223;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         40 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 99

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 159

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        160 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 219

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 279

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 339

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 399

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 459

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 519

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 579

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 639

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 699

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        700 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 759

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        760 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 813
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RESULT 3
AAN90126
ID AAN90126 standard; cDNA; 1088 BP.
XX
AC AAN90126;
XX
DT 24-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 01-NOV-1989 (first entry)
XX
DE cDNA encoding human mast cell IgE receptor alpha subunit.
XX
KW cDNA; immunoglobulin E receptor alpha subunit; treats allergies;
KW design non-peptide drugs; human.
XX
OS Homo sapiens; (Human); mast cell line.
OS KU812.
XX
FH Key Location/Qualifiers
FT CDS 35. .805
FT /*tag= a
XX
PN WO8905352-A.
XX
PD 15-JUN-1989.
XX
PF 29-NOV-1988; 88WO-US004255.
XX
PR 01-DEC-1987; 87US-00127214.
XX
PA (HARD) HARVARD COLLEGE.
PA (USSH) NAT INST OF HEALTH.
XX
PI Leder P, Benfey P;
XX
DR WPI; 1989-192698/26.
DR P-PSDB; AAP90385.
XX
PT CDNA encoding IGE receptor alpha-sub-unit - used to treat allergies.
XX
PS Disclosure; Fig 4; 17pp; English.
XX
CC cDNA sequence encoding immunoglobulin E receptor alpha subunit of human
CC mast cell IgE surface receptor (see corresp. AAP90385). Used to produce
CC antibodies which can diagnose IgE receptor levels, measure and treat
CC allergies, and design non-peptide drugs. (Updated on 25-MAR-2003 to
CC correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
XX
SQ Sequence 1088 BP; 347 A; 216 C; 229 G; 296 T; 0 U; 0 Other;

Query Match 100.0%; Score 774; DB 1; Length 1088;
Best Local Similarity 100.0%; Pred. No. 2.8e-223;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         35 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 94

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 154

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        155 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 214

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        215 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 274

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        275 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 334

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        335 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 394

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 454

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        455 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 514

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 574

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 634

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 694

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 754

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        755 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 808


RESULT 4
AAQ51020
ID   AAQ51020 standard; DNA; 1174 BP.
XX
AC   AAQ51020;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1994  (first entry)
XX
DE   Human FceRI alpha gene.
XX
KW   IgE; immunoglogulin E receptor; beta subunit; basophils; allergy;
KW   aggregation; signal transduction; diagnosis; antagonist; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             107. .881
FT                   /*tag=  a
XX
PN   WO9321317-A1.
XX
PD   28-OCT-1993.
XX
PF   16-APR-1993;   93WO-US003419.
XX
PR   16-APR-1992;   92US-00869933.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX
PI   Kinet JP;
XX
DR   WPI; 1993-351727/44.
DR   P-PSDB; AAR42336.
XX
PT   Immunoglobulin E receptor human beta sub-unit isolation - using 1st
PT   strand reverse transcripts from human basophils as templates for a
PT   polymerase chain reaction, used to treat and diagnose allergic diseases.
XX
PS   Claim 1; Fig 1; 154pp; English.
XX
CC   The sequence is that of the human FcRI alpha subunit, isolated by using
CC   first strand reverse transcriptase from human basophils by PCR. The gene
CC   and its prod. can be used to identify human beta subuit FceRI inhibitors
CC   (immunoglobulin E receptor) which inhibit the binding of IgE to its
CC   receptor and inhibit the aggragation function of the receptor or the
CC   signal transducing function related to allergic response. Such inhibitors
CC   can be used for the treatment or prevention of allergic disease. See also
CC   AAQ51021-4. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 1174 BP; 378 A; 240 C; 241 G; 315 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 774;  DB 2;  Length 1174;
  Best Local Similarity  100.0%;  Pred. No. 2.9e-223;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880


RESULT 5
AAT85615
ID   AAT85615 standard; cDNA; 1197 BP.
XX
AC   AAT85615;
XX
DT   04-FEB-1998  (first entry)
XX
DE   Alpha subunit of human high affinity receptor for IgE (human FcERI) cDNA.
XX
KW   alpha subunit; human high affinity receptor; IgE; FcERI; antigen;
KW   preformed mediator; histamine; serotonin; leukotriene; IgE level;
KW   allergic condition; therapy; allergic response; drug screening;
KW   DNA probe; diagnostic assay; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             106. .880
FT                   /*tag=  a
FT                   /product= "human_FcERI_alpha_subunit"
FT   sig_peptide     106. .181
FT                   /*tag=  b
FT   mat_peptide     182. .877
FT                   /*tag=  c
FT                   /product= "alpha_subunit"
XX
PN   US5639660-A.
XX
PD   17-JUN-1997.
XX
PF   24-FEB-1988;   88US-00160457.
XX
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PR   24-FEB-1988;   88US-00160457.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA   (HOFF ) HOFFMANN LA ROCHE INC.
XX
PI   Kochan JP,  Kinet JP;
XX
DR   WPI; 1997-332052/30.
DR   P-PSDB; AAW24066.
XX
PT   DNA encoding alpha sub-unit of high affinity receptor for immunoglobulin
PT   E - used for producing polypeptide(s) which can be used for therapy or to
PT   prevent allergic responses or in diagnostic and screening assays.
XX
PS   Claim 1; Fig 1A-B; 15pp; English.
XX
CC   This cDNA sequence encodes the alpha subunit of the human high affinity
CC   receptor for IgE (FcERI). FcERI is found exclusively on mast cells,
CC   basophils and related cells. Aggregation of IgE occupied FcERI by antigen
CC   triggers both the release of of preformed mediators such as histamine and
CC   serotonin, as well as stimulating the synthesis of leukotrienes. It is
CC   the release of these mediators that results in an allergic condition. The
CC   DNA can be used to produce the human FcERI alpha polypeptides which can
CC   be used for therapy or to prevent allergic responses, in drug screening
CC   assays or for monitoring IgE levels in patients. The DNA can also be used
CC   to produce DNA probes useful in diagnostic assays
XX
SQ   Sequence 1197 BP; 389 A; 242 C; 245 G; 321 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 774;  DB 2;  Length 1197;
  Best Local Similarity   100.0%;  Pred. No. 3e-223;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        106 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 165

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        166 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 225

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        226 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 285

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        286 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 345

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        346 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 405

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        406 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 465

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        466 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 525

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 585

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 645

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        646 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 705

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        706 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 765

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        766 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 825

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        826 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 879


RESULT 6
AAV36343
ID   AAV36343 standard; cDNA; 1198 BP.
XX
AC   AAV36343;
XX
DT   07-OCT-1998  (first entry)
XX
DE   cDNA encoding the alpha chain of a Fc epsilon receptor.
XX
KW   Alpha chain; human; Fc epsilon receptor; canine; equine; feline;
KW   immunoglobulin E; IgE; detection; diagnose; allergy; atopic disease;
KW   hyper-IgE syndrome; internal parasitic infection; B cell neoplasia;
KW   flea allergy; heartworm infection; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             107. .880
FT                   /*tag=  a
XX
PN   WO9823964-A1.
XX
PD   04-JUN-1998.
XX
PF   24-NOV-1997;   97WO-US021651.
XX
PR   26-NOV-1996;   96US-00756387.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Frank RG,  Porter JP,  Rushlow KE,  Wassom DL;
XX
DR   WPI; 1998-322873/28.
DR   P-PSDB; AAW61190.
XX
PT   Detection of non-human immunoglobulin E - by complex formation with human
PT   Fc epsilon receptor, used for, e.g. diagnosis of allergy and atopic
PT   disease.
XX
PS   Claim 11; Page 36-37; 70pp; English.
XX
CC   The present sequence encodes the alpha chain of the human Fc epsilon
CC   receptor. Detection of canine, equine or feline immunoglobulin E (IgE)
CC   comprises reacting isolated human Fc epsilon receptor with the test
CC   sample and detecting formation of a IgE-receptor complex. Detection of
CC   IgE is used to diagnose allergy, atopic disease, hyper-IgE syndrome,
CC   internal parasitic infections or B cell neoplasia, and for measuring
CC   effect of treatments. Most particularly flea allergy in dogs and cats is
CC   detected, and also heartworm infection
XX
SQ   Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 774;  DB 2;  Length 1198;
  Best Local Similarity   100.0%;  Pred. No. 3e-223;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166
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```
Qy          61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy         121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy         181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy         241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy         301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy         361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy         421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy         481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy         541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy         601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy         661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy         721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
               ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
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RESULT 7
AAA34813
ID AAA34813 standard; DNA; 1198 BP.
XX
AC AAA34813;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2502.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstruction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 655; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 774; DB 3; Length 1198;
Best Local Similarity 100.0%; Pred. No. 3e-223;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy           1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy          61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy         121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy         181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy         241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy         301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
```

RESULT 8
AAF20935
ID AAF20935 standard; DNA; 1198 BP.
XX
AC AAF20935;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human high affinity IgE receptor polynucleotide fragment #2502.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US008020.
XX
PR 06-APR-1999; 99US-0127958P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
PI Nyce JW;
XX
DR WPI; 2000-679539/66.
XX
PT Low adenosine (A) content antisense oligonucleotides which do not trigger
PT adenosine receptors during metabolism, useful e.g. for treating cancers
PT and respiratory obstructions.
XX
PS Disclosure; Page 138; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
CC surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
CC fragments and antisense oligonucleotides used in the exemplification of
CC the present invention
XX
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 774; DB 3; Length 1198;
Best Local Similarity 100.0%; Pred. No. 3e-223;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646
```

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Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
```

RESULT 9
AAF77692
ID AAF77692 standard; cDNA; 1198 BP.
XX
AC AAF77692;
XX
DT 29-MAY-2001 (first entry)
XX
DE Human wild-type FcepsilonRIalpha chain coding sequence.
XX
KW Human; FcepsilonRIbeta chain; immunoglobulin E; allergy; atopy;
KW conjunctivitis; rhinitis; anaphylaxis; urticaria; angioedema; ss.
XX
OS Homo sapiens.
XX
PN WO200121816-A1.
XX
PD 29-MAR-2001.
XX
PF 21-SEP-2000; 2000WO-US025877.
XX
PR 21-SEP-1999; 99US-0154924P.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Kinet J, Donnadieu E, Jouvin M, Cookson W, Moffatt MF;
XX
DR WPI; 2001-266077/27.
XX
PT Inhibiting expression of high affinity receptors for immunoglobulin (Ig)
PT E, in cell or in subject to treat atopy, anaphylaxis mediated by IgE, by
PT contacting cell or administering to subject, a FcERIbeta chain variant.
XX
PS Disclosure; Page 52; 55pp; English.
XX
CC The present invention describes a method of inhibiting the expression of
CC the FcepsilonRI receptor by contacting a cell expressing it with an
CC FcepsilonRIbeta chain variant. The Fcepsilon receptor is a high affinity
CC receptor for immunoglobulin E. The method is useful in the treatment of
CC allergic conditions such as rhinitis, conjunctivitis, atopy, anaphylaxis,
CC urticaria and angioedema. The present sequence is the wild-type human
CC FcepsilonRIalpha chain coding sequence
XX
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 774; DB 4; Length 1198;
Best Local Similarity 100.0%; Pred. No. 3e-223;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
```

RESULT 10
AAF24912/c
ID AAF24912 standard; DNA; 1198 BP.
XX
AC AAF24912;
XX
DT 30-APR-2001 (first entry)
XX
DE Complement sequence of a human Fc epsilon receptor alpha-chain gene.
XX
KW Fc epsilon receptor; FcepsilonR; immunoglobulin E; IgE; atopic disease;
KW luminescence inducing protein; allergy; hyper IgE syndrome;
KW internal parasite infection; B cell neoplasia; ss.
XX
OS Homo sapiens.
XX
PN WO200104310-A1.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US019070.
XX
PR 13-JUL-1999; 99US-0143612P.
PR 02-MAR-2000; 2000US-0186412P.
XX

PA (HESK-) HESKA CORP.
PA (PROM-) PROMEGA CORP.
XX
PI Weber ER, Wood KV, Hall MP;
XX
DR WPI; 2001-103082/11.
XX
PT A fusion protein, comprising an Fc epsilon receptor domain and a
PT luminescence inducing protein domain that induces a LP substrate to emit
PT light when contacted with the LP domain, useful for detecting
PT immunoglobulin (Ig) E.
XX
PS Example; Page 61; 105pp; English.
XX
CC The present sequence represents the complement of a human Fc epsilon
CC receptor (FcepsilonR) alpha-chain protein, that binds to immunoglobulin
CC (Ig) E). The FcepsilonR domain is used to produce a fusion protein, which
CC also comprises a luminescence inducing protein domain that induces a
CC substrate to emit light when contacted with the luminescence inducing
CC protein domain. The fusion protein may be used to detect IgE. It may also
CC be used to identify a compound capable of inhibiting FcepsilonR protein
CC activity. IgE antibody production is indicative of diseases such as
CC allergies, atopic disease, hyper IgE syndrome, internal parasite
CC infections and B cell neoplasia. Detection of IgE production in an animal
CC following therapy is indicative of the efficacy of the treatment, for
CC example when using treatments intended to disrupt IgE production
XX
SQ Sequence 1198 BP; 321 A; 245 C; 243 G; 389 T; 0 U; 0 Other;

Query Match 100.0%; Score 774; DB 5; Length 1198;
Best Local Similarity 100.0%; Pred. No. 3e-223;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1092 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 1033

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 973

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 913

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        912 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 853

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        852 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 793

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        792 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 733

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        732 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 673

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        672 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 613

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 553

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 493
```

```
Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 433

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 373

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 319
```

RESULT 11
AAF24911
ID AAF24911 standard; DNA; 1198 BP.
XX
AC AAF24911;
XX
DT 30-APR-2001 (first entry)
XX
DE Nucleotide sequence of a human Fc epsilon receptor alpha-chain.
XX
KW Fc epsilon receptor; FcepsilonR; immunoglobulin E; IgE; atopic disease;
KW luminescence inducing protein; allergy; hyper IgE syndrome;
KW internal parasite infection; B cell neoplasia; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 107. .880
FT /*tag= a
FT /product= "Fc epsilon receptor alpha-chain"
XX
PN WO200104310-A1.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US019070.
XX
PR 13-JUL-1999; 99US-0143612P.
PR 02-MAR-2000; 2000US-0186412P.
XX
PA (HESK-) HESKA CORP.
PA (PROM-) PROMEGA CORP.
XX
PI Weber ER, Wood KV, Hall MP;
XX
DR WPI; 2001-103082/11.
DR P-PSDB; AAB31584.
XX
PT A fusion protein, comprising an Fc epsilon receptor domain and a
PT luminescence inducing protein domain that induces a LP substrate to emit
PT light when contacted with the LP domain, useful for detecting
PT immunoglobulin (Ig) E.
XX
PS Claim 17; Page 58-59; 105pp; English.
XX
CC The present sequence encodes a human Fc epsilon receptor (FcepsilonR)
CC alpha-chain protein, that binds to immunoglobulin (Ig) E). The FcepsilonR
CC domain is used to produce a fusion protein, which also comprises a
CC luminescence inducing protein domain that induces a substrate to emit
CC light when contacted with the luminescence inducing protein domain. The
CC fusion protein may be used to detect IgE. It may also be used to identify
CC a compound capable of inhibiting FcepsilonR protein activity. IgE
CC antibody production is indicative of diseases such as allergies, atopic
CC disease, hyper IgE syndrome, internal parasite infections and B cell
CC neoplasia. Detection of IgE production in an animal following therapy is
CC indicative of the efficacy of the treatment, for example when using
CC treatments intended to disrupt IgE production
XX
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

```
  Query Match           100.0%;  Score 774;  DB 5;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 3e-223;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
```

RESULT 12
ABL67793
ID ABL67793 standard; DNA; 1198 BP.
XX
AC ABL67793;
XX
DT 15-MAY-2002 (first entry)
XX
DE Oesophagus cancer related gene sequence SEQ ID NO:6130.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200194629-A2.
XX
PD 13-DEC-2001.
XX
PF 30-MAY-2001; 2001WO-US010838.
XX
PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX
PA (AVAL-) AVALON PHARM.
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX
DR WPI; 2002-188264/24.
XX
PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
PS Claim 1; SEQ ID NO 6130; 44pp; English.
XX
CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result

```
CC   of M1, and the data is sufficient to convey the chemical structure and/or
CC   properties of the agent. M1 can be used in the treatment of cancer such
CC   as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC   prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC   cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC   cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
CC   tumour
XX
SQ   Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 774;  DB 6;  Length 1198;
  Best Local Similarity   100.0%;  Pred. No. 3e-223;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880


RESULT 13
ABZ96629
ID   ABZ96629 standard; DNA; 1198 BP.
XX
AC   ABZ96629;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human high affinity IgE receptor oligonucleotide fragment.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;.
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Disclosure; SEQ ID NO 11871; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 774;  DB 7;  Length 1198;
  Best Local Similarity   100.0%;  Pred. No. 3e-223;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286
```

```
Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
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Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
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RESULT 14
ADB85535
ID ADB85535 standard; cDNA; 1198 BP.
XX
AC ADB85535;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human immunoglobulin E high affinity receptor (FcERI) alpha subunit cDNA.
XX
KW alpha subunit; high affinity receptor for immunoglobulin E; FcERI;
KW mast cell; basophil; histamine; serotonin; allergic condition;
KW antiallergic; allergic response; drug screening assay; immunoglobulin E;
KW human; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   107. .880
FT   /*tag= a
FT   /product= "Human FcERI receptor"
FT   /transl_except= (767. .769, aa:Glu)
FT   /transl_except= (863. .865, aa:Asp)
XX
PN US6602983-B1.
XX
PD 05-AUG-2003.
XX
PF 22-SEP-1994; 94US-00310902.
XX
PR 24-FEB-1988; 88US-00160457.
PR 30-OCT-1991; 91US-00785127.
PR 29-MAY-1993; 93US-00066640.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinet JP, Kochan JP;
XX
DR WPI; 2003-669612/63.
DR P-PSDB; ADB85536.
XX
PT New alpha subunit of the human high affinity receptor for immunoglobulin
PT E polypeptides, useful as antagonists to prevent allergic response, as
PT reagents in drug screening assays, or for monitoring immunoglobulin E
PT levels in patients.
XX
PS Claim 1; Fig 1; 9pp; English.
XX
CC This invention relates to a novel purified polypeptide corresponding to
CC the alpha subunit of the human high affinity receptor for immunoglobulin
CC E (FcERI) and the DNA sequence which encodes it. The receptor of the
CC invention is found exclusively on mast cells, basophils and related
CC cells. Activation of the receptor triggers the release of preformed
CC mediators such as histamine and serotonin which may result in allergic
CC conditions. Compounds which modulate FcERI activity may have antiallergic
CC activity. The polypeptide of the invention may be useful as an antagonist
CC for preventing allergic response, as a reagent in drug screening assays,
CC as a therapeutic or for monitoring immunoglobulin E levels in patients.
CC The DNA sequences may be useful for producing the polypeptide or for
CC synthesising cDNA sequences to construct DNA probes used in diagnostic
CC assays. The present sequence is the cDNA sequence encoding the alpha
CC subunit of the human FcERI receptor of the invention.
XX
SQ Sequence 1198 BP; 389 A; 243 C; 245 G; 321 T; 0 U; 0 Other;

Query Match 100.0%; Score 774; DB 9; Length 1198;
Best Local Similarity 100.0%; Pred. No. 3e-223;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
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Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
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Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646
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Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
```

RESULT 15
AAA34816
ID AAA34816 standard; DNA; 21742 BP.
XX
AC AAA34816;
XX
DT 28-JUL-2000 (first entry)
XX
DE Human adenosine receptor related polynucleotide SEQ ID NO:2505.
XX
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX
OS Homo sapiens.
XX
PN WO200009525-A2.
XX
PD 24-FEB-2000.
XX
PF 03-AUG-1999; 99WO-US017712.
XX
PR 03-AUG-1998; 98US-0095212P.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
PI Nyce JW;
XX
DR WPI; 2000-205971/18.
XX
PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstruction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX
PS Disclosure; Page 658-664; 1343pp; English.
XX
CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX
SQ Sequence 21742 BP; 6598 A; 4107 C; 4408 G; 6612 T; 0 U; 17 Other;

  Query Match   100.0%; Score 774; DB 3; Length 21742;
  Best Local Similarity 100.0%; Pred. No. 1.3e-222;
  Matches 774; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8459 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 8518

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8519 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 8578

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8579 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 8638

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8639 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 8698

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8699 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 8758

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8759 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 8818

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8819 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 8878

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8879 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 8938

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8939 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 8998

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       8999 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 9058

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9059 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 9118

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9119 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 9178

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9179 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 9232
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Search completed: October 8, 2004, 23:17:38

Job time : 377.347 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	774	100.0	774	2	US-08-756-387B-4	Sequence 4, Appli
c 2	774	100.0	774	2	US-08-756-387B-5	Sequence 5, Appli
3	774	100.0	774	4	US-09-285-873-4	Sequence 4, Appli
c 4	774	100.0	774	4	US-09-285-873-5	Sequence 5, Appli
5	774	100.0	774	4	US-09-944-277A-4	Sequence 4, Appli
c 6	774	100.0	774	4	US-09-944-277A-5	Sequence 5, Appli
7	774	100.0	1174	1	US-07-869-933-10	Sequence 10, Appl
8	774	100.0	1174	3	US-09-103-663-10	Sequence 10, Appl
9	774	100.0	1198	2	US-08-756-387B-1	Sequence 1, Appli
c 10	774	100.0	1198	2	US-08-756-387B-3	Sequence 3, Appli
11	774	100.0	1198	4	US-09-285-873-1	Sequence 1, Appli
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13	774	100.0	1198	4	US-09-944-277A-1	Sequence 1, Appli
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15	773	99.9	773	4	US-08-897-956A-6	Sequence 6, Appli
16	699	90.3	699	2	US-08-756-387B-7	Sequence 7, Appli
17	699	90.3	699	4	US-09-285-873-7	Sequence 7, Appli
18	699	90.3	699	4	US-09-944-277A-7	Sequence 7, Appli
19	611	78.9	2955	4	US-08-897-956A-4	Sequence 4, Appli
20	591	76.4	591	2	US-08-756-387B-10	Sequence 10, Appl
21	591	76.4	591	4	US-09-285-873-10	Sequence 10, Appl
22	591	76.4	591	4	US-09-944-277A-10	Sequence 10, Appl
23	591	76.4	713	2	US-08-238-027-3	Sequence 3, Appli
24	589.4	76.1	591	3	US-08-788-954-1	Sequence 1, Appli
25	516	66.7	516	2	US-08-756-387B-12	Sequence 12, Appl
26	516	66.7	516	4	US-09-285-873-12	Sequence 12, Appl
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c 29	438.4	56.6	1015	3	US-09-015-734-3	Sequence 3, Appli
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c 35	435	56.2	765	4	US-09-515-311-5	Sequence 5, Appli
36	403.8	52.2	708	3	US-09-015-734-6	Sequence 6, Appli
c 37	403.8	52.2	708	3	US-09-015-734-8	Sequence 8, Appli
38	403.8	52.2	708	4	US-09-515-311-6	Sequence 6, Appli
c 39	403.8	52.2	708	4	US-09-515-311-8	Sequence 8, Appli
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c 45	400	51.7	1069	3	US-09-515-431-3	Sequence 3, Appli

ALIGNMENTS

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RESULT 1
US-08-756-387B-4
; Sequence 4, Application US/08756387B
; Patent No. 5945294
;  GENERAL INFORMATION:
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Porter, James P.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wassom, Donald L.
;    TITLE OF INVENTION:  Method to Detect IgE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carol Talkington Verser, Ph.D.
;      ADDRESSEE:  Heska Corporation
;      STREET:  1825 Sharp Point Drive
;      CITY:  Fort Collins
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80525
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect for Windows, Version 7.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/756,387B
;      FILING DATE:  No. 5945294ember 26, 1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Verser, Carol Talkington
;      REGISTRATION NUMBER:  37,459
;      REFERENCE/DOCKET NUMBER:  DI-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  970/493-7272
;      TELEFAX:  970/484-9505
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  774 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..774
US-08-756-387B-4

  Query Match           100.0%;  Score 774;  DB 2;  Length 774;
  Best Local Similarity  100.0%;  Pred. No. 5.2e-246;
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Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
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Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
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Db        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
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Db        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
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RESULT 2
US-08-756-387B-5/c
; Sequence 5, Application US/08756387B
; Patent No. 5945294
;  GENERAL INFORMATION:
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Porter, James P.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wassom, Donald L.
;    TITLE OF INVENTION:  Method to Detect IgE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carol Talkington Verser, Ph.D.
;      ADDRESSEE:  Heska Corporation
;      STREET:  1825 Sharp Point Drive
;      CITY:  Fort Collins
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80525
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect for Windows, Version 7.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/756,387B
;      FILING DATE:  No. 5945294ember 26, 1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Verser, Carol Talkington
;      REGISTRATION NUMBER:  37,459
;      REFERENCE/DOCKET NUMBER:  DI-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  970/493-7272
;      TELEFAX:  970/484-9505
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  774 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-756-387B-5

  Query Match             100.0%;  Score 774;  DB 2;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-246;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 715

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 655

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 595

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 535

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 475

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 415

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 355

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 295

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 235

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 175

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 115
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Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 55

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         54 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 1


RESULT 3
US-09-285-873-4
; Sequence 4, Application US/09285873
; Patent No. 6309832
;  GENERAL INFORMATION:
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Porter, James P.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wassom, Donald L.
;    TITLE OF INVENTION:  Method to Detect IgE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carol Talkington Verser, Ph.D.
;      ADDRESSEE:  Heska Corporation
;      STREET:  1825 Sharp Point Drive
;      CITY:  Fort Collins
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80525
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect for Windows, Version 7.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/285,873
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/756,387
;      FILING DATE:  No. 6309832ember 26, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Verser, Carol Talkington
;      REGISTRATION NUMBER:  37,459
;      REFERENCE/DOCKET NUMBER:  DI-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  970/493-7272
;      TELEFAX:  970/484-9505
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  774 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..774
US-09-285-873-4

  Query Match             100.0%;  Score 774;  DB 4;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-246;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
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Db          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Db        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
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Db        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
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Db        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
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Db        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
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Db        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774


RESULT 4
US-09-285-873-5/c
; Sequence 5, Application US/09285873
; Patent No. 6309832
;  GENERAL INFORMATION:
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Porter, James P.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wassom, Donald L.
;    TITLE OF INVENTION:  Method to Detect IgE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carol Talkington Verser, Ph.D.
;      ADDRESSEE:  Heska Corporation
;      STREET:  1825 Sharp Point Drive
;      CITY:  Fort Collins
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80525
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect for Windows, Version 7.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/285,873
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/756,387
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;      FILING DATE:  No. 6309832ember 26, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Verser, Carol Talkington
;      REGISTRATION NUMBER:  37,459
;      REFERENCE/DOCKET NUMBER:  DI-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  970/493-7272
;      TELEFAX:  970/484-9505
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  774 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-285-873-5

  Query Match           100.0%;  Score 774;  DB 4;  Length 774;
  Best Local Similarity  100.0%;  Pred. No. 5.2e-246;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
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Db        774 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 715

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
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Db        714 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 655

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Db        654 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 595

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 535

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 475

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 415

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 355

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 295

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 235

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 175

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 115

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 55

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         54 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 1
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RESULT 5
US-09-944-277A-4
; Sequence 4, Application US/09944277A
; Patent No. 6682894
;   GENERAL INFORMATION:
;        APPLICANT: Frank, Glenn R.
;                   Porter, James P.
;                   Rushlow, Keith E.
;                   Wassom, Donald L.
;        TITLE OF INVENTION: Method to Detect IgE
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Carol Talkington Verser, Ph.D.
;                        Heska Corporation
;             STREET: 1825 Sharp Point Drive
;             CITY: Fort Collins
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80525
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: WordPerfect for Windows, Version 7.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/944,277A
;             FILING DATE: 30-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/285,873
;             FILING DATE: 1999-03-31
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Verser, Carol Talkington
;             REGISTRATION NUMBER: 37,459
;             REFERENCE/DOCKET NUMBER: DI-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 970/493-7272
;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 774 nucleotides
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:   CDS
;             LOCATION:   1..774
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-944-277A-4

  Query Match           100.0%;  Score 774;  DB 4;  Length 774;
  Best Local Similarity  100.0%;  Pred. No. 5.2e-246;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Db        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
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Db        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
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Db        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774


RESULT 6
US-09-944-277A-5/c
; Sequence 5, Application US/09944277A
; Patent No. 6682894
;  GENERAL INFORMATION:
;       APPLICANT: Frank, Glenn R.
;                  Porter, James P.
;                  Rushlow, Keith E.
;                  Wassom, Donald L.
;       TITLE OF INVENTION: Method to Detect IgE
;       NUMBER OF SEQUENCES: 13
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Carol Talkington Verser, Ph.D.
;                       Heska Corporation
;            STREET: 1825 Sharp Point Drive
;            CITY: Fort Collins
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80525
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: Windows 95
;            SOFTWARE: WordPerfect for Windows, Version 7.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/944,277A
;            FILING DATE: 30-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/285,873
;            FILING DATE: 1999-03-31
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Verser, Carol Talkington
;            REGISTRATION NUMBER: 37,459
;            REFERENCE/DOCKET NUMBER: DI-1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 970/493-7272
;            TELEFAX: 970/484-9505
;  INFORMATION FOR SEQ ID NO: 5:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 774 nucleotides
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-944-277A-5

  Query Match            100.0%;  Score 774;  DB 4;  Length 774;
  Best Local Similarity  100.0%;  Pred. No. 5.2e-246;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 715

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 655

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 595

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 535

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 475

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 415

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 355

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 295

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 235

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 175

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 115

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 55

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         54 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 1


RESULT 7
US-07-869-933-10
; Sequence 10, Application US/07869933
; Patent No. 5770396
;  GENERAL INFORMATION:
```

```
;    APPLICANT:  KINET, Jean-Pierre
;    TITLE OF INVENTION:  ISOLATION, CHARACTERIZATION, AND USE OF
;    TITLE OF INVENTION:  THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
;    TITLE OF INVENTION:  IMMUNOGLOBULIN
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/869,933
;      FILING DATE:  19920416
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  40399/154 NIHD
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1174 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  107..880
US-07-869-933-10

  Query Match           100.0%;  Score 774;  DB 1;  Length 1174;
  Best Local Similarity  100.0%;  Pred. No. 6.8e-246;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880


RESULT 8
US-09-103-663-10
; Sequence 10, Application US/09103663D
; Patent No. 6171803
; GENERAL INFORMATION:
;  APPLICANT: Kinet et al.
;  TITLE OF INVENTION: Isolation, characterization, and use of the human beta
;  TITLE OF INVENTION: subunit of the high affinity receptor for
;  TITLE OF INVENTION: immunoglobulin E.
;  FILE REFERENCE: 50490
;  CURRENT APPLICATION NUMBER: US/09/103,663D
;  CURRENT FILING DATE: 1998-06-23
;  EARLIER APPLICATION NUMBER: 07/869,933
;  EARLIER FILING DATE: 1992-04-16
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 1174
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (107)..(880)
US-09-103-663-10

  Query Match           100.0%;  Score 774;  DB 3;  Length 1174;
  Best Local Similarity  100.0%;  Pred. No. 6.8e-246;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406
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Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
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RESULT 9
US-08-756-387B-1
; Sequence 1, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..877
US-08-756-387B-1

Query Match 100.0%; Score 774; DB 2; Length 1198;
Best Local Similarity 100.0%; Pred. No. 6.8e-246;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
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RESULT 10
US-08-756-387B-3/c
; Sequence 3, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.

```
;    APPLICANT:  Wassom, Donald L.
;    TITLE OF INVENTION:  Method to Detect IgE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carol Talkington Verser, Ph.D.
;      ADDRESSEE:  Heska Corporation
;      STREET:  1825 Sharp Point Drive
;      CITY:  Fort Collins
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80525
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect for Windows, Version 7.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/756,387B
;      FILING DATE:  No. 5945294ember 26, 1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Verser, Carol Talkington
;      REGISTRATION NUMBER:  37,459
;      REFERENCE/DOCKET NUMBER:  DI-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  970/493-7272
;      TELEFAX:  970/484-9505
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1198 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-756-387B-3

  Query Match           100.0%;  Score 774;  DB 2;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 6.8e-246;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1092 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 1033

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 973

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 913

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        912 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 853

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        852 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 793

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        792 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 733

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        732 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 673

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        672 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 613

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 553

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 493

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 433

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 373

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 319


RESULT 11
US-09-285-873-1
; Sequence 1, Application US/09285873
; Patent No. 6309832
;  GENERAL INFORMATION:
;    APPLICANT:  Frank, Glenn R.
;    APPLICANT:  Porter, James P.
;    APPLICANT:  Rushlow, Keith E.
;    APPLICANT:  Wassom, Donald L.
;    TITLE OF INVENTION:  Method to Detect IgE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carol Talkington Verser, Ph.D.
;      ADDRESSEE:  Heska Corporation
;      STREET:  1825 Sharp Point Drive
;      CITY:  Fort Collins
;      STATE:  Colorado
;      COUNTRY:  USA
;      ZIP:  80525
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  WordPerfect for Windows, Version 7.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/285,873
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/756,387
;      FILING DATE:  No. 6309832ember 26, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Verser, Carol Talkington
;      REGISTRATION NUMBER:  37,459
;      REFERENCE/DOCKET NUMBER:  DI-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  970/493-7272
;      TELEFAX:  970/484-9505
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1198 nucleotides
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  107..877
US-09-285-873-1

  Query Match           100.0%;  Score 774;  DB 4;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 6.8e-246;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
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RESULT 12
US-09-285-873-3/c
; Sequence 3, Application US/09285873
; Patent No. 6309832
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,873
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387
; FILING DATE: No. 6309832ember 26, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-285-873-3

Query Match 100.0%; Score 774; DB 4; Length 1198;
Best Local Similarity 100.0%; Pred. No. 6.8e-246;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
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Db       1092 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 1033

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 973

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 913

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
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Db        912 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 853

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        852 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 793

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        792 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 733

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        732 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 673

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        672 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 613

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 553

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 493

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
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Db        492 AAGTACTGGCTACAATTTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 433

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 373

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 319


RESULT 13
US-09-944-277A-1
; Sequence 1, Application US/09944277A
; Patent No. 6682894
;   GENERAL INFORMATION:
;        APPLICANT: Frank, Glenn R.
;                   Porter, James P.
;                   Rushlow, Keith E.
;                   Wassom, Donald L.
;        TITLE OF INVENTION: Method to Detect IgE
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Carol Talkington Verser, Ph.D.
;                        Heska Corporation
;             STREET: 1825 Sharp Point Drive
;             CITY: Fort Collins
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80525
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: WordPerfect for Windows, Version 7.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/944,277A
;             FILING DATE: 30-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/285,873
;             FILING DATE: 1999-03-31
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Verser, Carol Talkington
;             REGISTRATION NUMBER: 37,459
;             REFERENCE/DOCKET NUMBER: DI-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 970/493-7272
;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1198 nucleotides
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:   CDS
;             LOCATION:   107..877
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-944-277A-1

  Query Match           100.0%;  Score 774;  DB 4;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 6.8e-246;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880


RESULT 14
US-09-944-277A-3/c
; Sequence 3, Application US/09944277A
; Patent No. 6682894
;   GENERAL INFORMATION:
;        APPLICANT: Frank, Glenn R.
;                   Porter, James P.
;                   Rushlow, Keith E.
;                   Wassom, Donald L.
;        TITLE OF INVENTION: Method to Detect IgE
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Carol Talkington Verser, Ph.D.
;                        Heska Corporation
;             STREET: 1825 Sharp Point Drive
;             CITY: Fort Collins
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80525
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: WordPerfect for Windows, Version 7.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/944,277A
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; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-944-277A-3

Query Match 100.0%; Score 774; DB 4; Length 1198;
Best Local Similarity 100.0%; Pred. No. 6.8e-246;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 15
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; Sequence 6, Application US/08897956A
; Patent No. 6423512
; GENERAL INFORMATION:
; APPLICANT: Mary Ellen Digan
; APPLICANT: Philip Lake
; APPLICANT: Hermann Gram
; TITLE OF INVENTION: Fusion Polypeptides
; FILE REFERENCE: 600-7244/CPA
; CURRENT APPLICATION NUMBER: US/08/897,956A
; CURRENT FILING DATE: 1997-07-21
; PRIOR APPLICATION NUMBER: 60/022,689
; PRIOR FILING DATE: 1996-07-26
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion Polynucleotide
US-08-897-956A-6

Query Match 99.9%; Score 773; DB 4; Length 773;
Best Local Similarity 100.0%; Pred. No. 1.1e-245;
Matches 773; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 69.4267 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 10, 2004, 11:20:22 ; Search time 450.92 Seconds
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8701.874 Million cell updates/sec

Title: US-10-763-400-4
Perfect score: 774
Sequence: 1 atggctcctgccatggaatc.....caaaccccaaaaacaactga 774

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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c	2	774	100.0	774	9	US-09-944-277A-5	Sequence 5, Appli
	3	774	100.0	1198	9	US-09-944-277A-1	Sequence 1, Appli
c	4	774	100.0	1198	9	US-09-944-277A-3	Sequence 3, Appli
	5	774	100.0	1198	9	US-09-962-832-244	Sequence 244, App
	6	774	100.0	1198	17	US-10-775-169-141	Sequence 141, App
	7	772.4	99.8	898	13	US-10-236-392-27	Sequence 27, Appl
	8	699	90.3	699	9	US-09-944-277A-7	Sequence 7, Appli
	9	591	76.4	591	9	US-09-944-277A-10	Sequence 10, Appl
	10	530	68.5	757	13	US-10-236-392-29	Sequence 29, Appl
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	13	516	66.7	516	9	US-09-944-277A-12	Sequence 12, Appl
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	20	403.8	52.2	708	16	US-10-434-817-6	Sequence 6, Appli
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	22	329.8	42.6	603	16	US-10-434-817-11	Sequence 11, Appl
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	32	163	21.1	1977	13	US-10-240-425-1268	Sequence 1268, Ap
	33	163	21.1	1977	13	US-10-342-887-382	Sequence 382, App
	34	163	21.1	1977	13	US-10-172-118-382	Sequence 382, App
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	37	141.6	18.3	1318	12	US-10-152-319A-2037	Sequence 2037, Ap
	38	141.6	18.3	1318	16	US-10-191-803-266	Sequence 266, App
	39	140	18.1	1341	16	US-10-388-934-244	Sequence 244, App
	40	139.6	18.0	1321	12	US-09-836-544-22	Sequence 22, Appl
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ALIGNMENTS

RESULT 1
US-09-944-277A-4
; Sequence 4, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272

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;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 774 nucleotides
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:   CDS
;             LOCATION:   1..774
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-944-277A-4

  Query Match             100.0%;  Score 774;  DB 9;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-244;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
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Db          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60

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RESULT 2
US-09-944-277A-5/c
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; Sequence 5, Application US/09944277A
; Patent No. US20020034771A1
;   GENERAL INFORMATION:
;        APPLICANT: Frank, Glenn R.
;                   Porter, James P.
;                   Rushlow, Keith E.
;                   Wassom, Donald L.
;        TITLE OF INVENTION: Method to Detect IgE
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Carol Talkington Verser, Ph.D.
;                        Heska Corporation
;             STREET: 1825 Sharp Point Drive
;             CITY: Fort Collins
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80525
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: WordPerfect for Windows, Version 7.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/944,277A
;             FILING DATE: 30-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/285,873
;             FILING DATE: 1999-03-31
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Verser, Carol Talkington
;             REGISTRATION NUMBER: 37,459
;             REFERENCE/DOCKET NUMBER: DI-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 970/493-7272
;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 774 nucleotides
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-944-277A-5

  Query Match             100.0%;  Score 774;  DB 9;  Length 774;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-244;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        774 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 715

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 655

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 595

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 535

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 475

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 415
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Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 355

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 295

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 235

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 175

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 115

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 55

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         54 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 1
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RESULT 3
US-09-944-277A-1
; Sequence 1, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.
; Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect IgE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; Heska Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/944,277A
; FILING DATE: 30-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/285,873
; FILING DATE: 1999-03-31
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1198 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 107..877
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-944-277A-1

Query Match 100.0%; Score 774; DB 9; Length 1198;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
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RESULT 4
US-09-944-277A-3/c
; Sequence 3, Application US/09944277A
; Patent No. US20020034771A1
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; Porter, James P.
; Rushlow, Keith E.

```
;                Wassom, Donald L.
;       TITLE OF INVENTION: Method to Detect IgE
;       NUMBER OF SEQUENCES: 13
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Carol Talkington Verser, Ph.D.
;                       Heska Corporation
;            STREET: 1825 Sharp Point Drive
;            CITY: Fort Collins
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80525
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: Windows 95
;            SOFTWARE: WordPerfect for Windows, Version 7.0
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/944,277A
;            FILING DATE: 30-Aug-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/285,873
;            FILING DATE: 1999-03-31
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Verser, Carol Talkington
;            REGISTRATION NUMBER: 37,459
;            REFERENCE/DOCKET NUMBER: DI-1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 970/493-7272
;            TELEFAX: 970/484-9505
;  INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1198 nucleotides
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-944-277A-3

  Query Match           100.0%;  Score 774;  DB 9;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 1e-243;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1092 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 1033

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1032 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 973

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        972 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 913

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        912 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 853

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        852 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 793

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        792 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 733

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        732 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 673

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        672 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 613

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 553

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 493

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 433

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 373

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 319


RESULT 5
US-09-962-832-244
; Sequence 244, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
;  APPLICANT: Ebner, Reinhard
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
;  TITLE OF INVENTION:  Sets
;  FILE REFERENCE: 689290-74
;  CURRENT APPLICATION NUMBER: US/09/962,832
;  CURRENT FILING DATE:  2001-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,077
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: US/60/235,280
;  PRIOR FILING DATE: 2000-09-25
;  NUMBER OF SEQ ID NOS: 259
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 244
;   LENGTH: 1198
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-962-832-244

  Query Match           100.0%;  Score 774;  DB 9;  Length 1198;
  Best Local Similarity  100.0%;  Pred. No. 1e-243;
  Matches  774;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
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Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
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RESULT 6
US-10-775-169-141
; Sequence 141, Application US/10775169
; Publication No. US20040175743A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dorner, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
; LENGTH: 1198
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-775-169-141

Query Match 100.0%; Score 774; DB 17; Length 1198;
Best Local Similarity 100.0%; Pred. No. 1e-243;
Matches 774; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        107 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 166

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        167 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 226

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        227 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 286

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        287 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 346

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 406

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 466

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 526

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 586

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 646

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 706

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 766

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        767 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 826

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        827 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 880
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RESULT 7
US-10-236-392-27
; Sequence 27, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei
; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladamir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRochelle, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME

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;  FILE REFERENCE: 21402-442A
;  CURRENT APPLICATION NUMBER: US/10/236,392
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US09/540,763
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: US60/390,155
;  PRIOR FILING DATE: 2002-06-19
;  PRIOR APPLICATION NUMBER: US09/635,949
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: US60/318,765
;  PRIOR FILING DATE: 2001-09-12
;  PRIOR APPLICATION NUMBER: US60/357,303
;  PRIOR FILING DATE: 2002-02-15
;  PRIOR APPLICATION NUMBER: US60/367,753
;  PRIOR FILING DATE: 2002-03-25
;  PRIOR APPLICATION NUMBER: US60/369,479
;  PRIOR FILING DATE: 2002-04-02
;  PRIOR APPLICATION NUMBER: US09/659,634
;  PRIOR FILING DATE: 2000-09-12
;  PRIOR APPLICATION NUMBER: US60/318,120
;  PRIOR FILING DATE: 2001-09-07
;  PRIOR APPLICATION NUMBER: US60/318,130
;  PRIOR FILING DATE: 2001-09-07
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 794
;  SOFTWARE: Custom
; SEQ ID NO 27
;    LENGTH: 898
;    TYPE: DNA
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (26)..(797)
US-10-236-392-27

  Query Match            99.8%;  Score 772.4;  DB 13;  Length 898;
  Best Local Similarity  99.9%;  Pred. No. 2.9e-243;
  Matches  773;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        -26 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 85

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 145

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 205

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 265

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 325

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 385

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 445

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        446 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 505

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 565

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 625

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        626 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 685

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        686 GGATTATTTATCTCAACCCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 745

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        746 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 799


RESULT 8
US-09-944-277A-7
; Sequence 7, Application US/09944277A
; Patent No. US20020034771A1
;   GENERAL INFORMATION:
;        APPLICANT: Frank, Glenn R.
;                   Porter, James P.
;                   Rushlow, Keith E.
;                   Wassom, Donald L.
;        TITLE OF INVENTION: Method to Detect IgE
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Carol Talkington Verser, Ph.D.
;                        Heska Corporation
;             STREET: 1825 Sharp Point Drive
;             CITY: Fort Collins
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80525
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: WordPerfect for Windows, Version 7.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/944,277A
;             FILING DATE: 30-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/285,873
;             FILING DATE: 1999-03-31
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Verser, Carol Talkington
;             REGISTRATION NUMBER: 37,459
;             REFERENCE/DOCKET NUMBER: DI-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 970/493-7272
;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 7:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 699 nucleotides
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:   CDS
;             LOCATION:   1..699
;        SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-944-277A-7

  Query Match            90.3%;  Score 699;  DB 9;  Length 699;
  Best Local Similarity  100.0%;  Pred. No. 3.9e-219;
  Matches  699;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy         76 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 60

Qy        136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 120

Qy        196 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 180

Qy        256 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240

Qy        316 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 300

Qy        376 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 360

Qy        436 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 420

Qy        496 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 480

Qy        556 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAA 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAA 540

Qy        616 TTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCA 675
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCA 600

Qy        676 ACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTT 735
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 ACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTT 660

Qy        736 CTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              |||||||||||||||||||||||||||||||||||||||
Db        661 CTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 699
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RESULT 9
US-09-944-277A-10
; Sequence 10, Application US/09944277A
; Patent No. US20020034771A1
;   GENERAL INFORMATION:
;        APPLICANT: Frank, Glenn R.
;                   Porter, James P.
;                   Rushlow, Keith E.
;                   Wassom, Donald L.
;        TITLE OF INVENTION: Method to Detect IgE
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Carol Talkington Verser, Ph.D.
;                        Heska Corporation
;             STREET: 1825 Sharp Point Drive
;             CITY: Fort Collins
;             STATE: Colorado
;             COUNTRY: USA
;             ZIP: 80525
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: WordPerfect for Windows, Version 7.0
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/944,277A
;             FILING DATE: 30-Aug-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/285,873
;             FILING DATE: 1999-03-31
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Verser, Carol Talkington
;             REGISTRATION NUMBER: 37,459
;             REFERENCE/DOCKET NUMBER: DI-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 970/493-7272
;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 nucleotides
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:   CDS
;             LOCATION:   1..591
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-944-277A-10

  Query Match             76.4%;  Score 591;  DB 9;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-183;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCT 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCT 591
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RESULT 10
US-10-236-392-29
; Sequence 29, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
;  APPLICANT: Anderson, David W
;  APPLICANT:  Boldog, Ferenc L
;  APPLICANT:  Burgess, Catherine, E
;  APPLICANT:  Casman, Stacie J
;  APPLICANT:  Catterton, Elina
;  APPLICANT:  Chapoval, Andrei
;  APPLICANT:  Crabtree, Julie
;  APPLICANT:  Edinger, Shlomit, R
;  APPLICANT:  Ellerman, Karen
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Gorman, Linda
;  APPLICANT:  Grosse, William M
;  APPLICANT:  Gusev, Vladamir
;  APPLICANT:  Kekuda, Ramesh
;  APPLICANT:  LaRochelle, William J
;  APPLICANT:  Li, Li
;  APPLICANT:  MacDougall, John R
;  APPLICANT:  Malyankar, Uriel M
;  APPLICANT:  Miller, Charles E
;  APPLICANT:  Millet, Isabelle
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Pena, Carol A
;  APPLICANT:  Peyman, John A
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Reiger, Daniel K
;  APPLICANT:  Rothenberg, Mark E
;  APPLICANT:  Shenoy, Suresh
;  APPLICANT:  Shimkets, Richard A
;  APPLICANT:  Smithson, Glennda
;  TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
;  FILE REFERENCE: 21402-442A
;  CURRENT APPLICATION NUMBER: US/10/236,392
;  CURRENT FILING DATE:  2002-09-06
;  PRIOR APPLICATION NUMBER: US09/540,763
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: US60/390,155
;  PRIOR FILING DATE: 2002-06-19
;  PRIOR APPLICATION NUMBER: US09/635,949
;  PRIOR FILING DATE: 2000-08-10
;  PRIOR APPLICATION NUMBER: US60/318,765
;  PRIOR FILING DATE: 2001-09-12
;  PRIOR APPLICATION NUMBER: US60/357,303
;  PRIOR FILING DATE: 2002-02-15
;  PRIOR APPLICATION NUMBER: US60/367,753
;  PRIOR FILING DATE: 2002-03-25
;  PRIOR APPLICATION NUMBER: US60/369,479
;  PRIOR FILING DATE: 2002-04-02
;  PRIOR APPLICATION NUMBER: US09/659,634
;  PRIOR FILING DATE: 2000-09-12
;  PRIOR APPLICATION NUMBER: US60/318,120
;  PRIOR FILING DATE: 2001-09-07
;  PRIOR APPLICATION NUMBER: US60/318,130
;  PRIOR FILING DATE: 2001-09-07
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 794
;  SOFTWARE: Custom
; SEQ ID NO 29
;   LENGTH: 757
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (26)..(680)
US-10-236-392-29

  Query Match            68.5%;  Score 530;  DB 13;  Length 757;
  Best Local Similarity  84.9%;  Pred. No. 2.1e-163;
  Matches  657;  Conservative    0;  Mismatches    0;  Indels  117;  Gaps    1;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 85

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 145

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 205

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 265

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAA---------------------------- 301

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 ------------------------------------------------------------ 301

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
                                                  ||||||||||||||||||||||||||||
Db        302 ----------------------------------TGCCATGGTTGGAGGAACTGGGATGTG 328

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 388

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 448

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        449 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 508

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        509 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACA 568

Qy        661 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        569 GGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGG 628

Qy        721 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        629 AAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 682


RESULT 11
US-09-809-715-1
; Sequence 1, Application US/09809715
; Publication No. US20030003502A1
; GENERAL INFORMATION:
;  APPLICANT: Jardetzky, Theodore S.
;  APPLICANT:  Garman, Scott Clayton
;  APPLICANT:  Wurzburg, Beth A.
;  APPLICANT:  Kinet, Jean-Pierre
;  TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A Fc
;  TITLE OF INVENTION:  EPSILON RECEPTOR ALPHA CHAIN AND A Fc REGION OF AN IgE
;  TITLE OF INVENTION:  ANTIBODY AND USES THEREOF
;  FILE REFERENCE: AL-8
;  CURRENT APPLICATION NUMBER: US/09/809,715
;  CURRENT FILING DATE:  2001-03-14
;  PRIOR APPLICATION NUMBER: 60/189,853
;  PRIOR FILING DATE: 2000-03-15
;  NUMBER OF SEQ ID NOS: 6
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;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 528
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(528)
US-09-809-715-1

  Query Match            68.2%;  Score 528;  DB 10;  Length 528;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-163;
  Matches  528;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          76 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 135
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 60

Qy         136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 195
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 120

Qy         196 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 255
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 180

Qy         256 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 315
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240

Qy         316 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 375
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 300

Qy         376 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 435
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 360

Qy         436 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 495
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 420

Qy         496 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 555
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 480

Qy         556 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAG 603
               |||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAG 528


RESULT 12
US-10-293-992-1
; Sequence 1, Application US/10293992
; Publication No. US20040033527A1
; GENERAL INFORMATION:
;  APPLICANT: Jardetzky, Theodore S.
;  APPLICANT:  Garman, Scott Clayton
;  APPLICANT:  Kinet, Jean-Pierre
;  TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A Fc EPSILON RECEPT
;  TITLE OF INVENTION:  CHAIN
;  FILE REFERENCE: AL-3-C1-1
;  CURRENT APPLICATION NUMBER: US/10/293,992
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: 09/434,193
;  PRIOR FILING DATE: 1999-11-04
;  PRIOR APPLICATION NUMBER: 60/107,219
;  PRIOR FILING DATE: 1998-11-05
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 528
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(528)
;   OTHER INFORMATION:
US-10-293-992-1

  Query Match            68.2%;  Score 528;  DB 13;  Length 528;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-163;
  Matches  528;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          76 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 135
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 60

Qy         136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 195
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 120

Qy         196 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 255
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 180

Qy         256 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 315
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240

Qy         316 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 375
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 300

Qy         376 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 435
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 360

Qy         436 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 495
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 420

Qy         496 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 555
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         421 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 480

Qy         556 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAG 603
               |||||||||||||||||||||||||||||||||||||||||||||||
Db         481 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAG 528


RESULT 13
US-09-944-277A-12
; Sequence 12, Application US/09944277A
; Patent No. US20020034771A1
;  GENERAL INFORMATION:
;       APPLICANT: Frank, Glenn R.
;                  Porter, James P.
;                  Rushlow, Keith E.
;                  Wassom, Donald L.
;       TITLE OF INVENTION: Method to Detect IgE
;       NUMBER OF SEQUENCES: 13
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Carol Talkington Verser, Ph.D.
;                       Heska Corporation
;            STREET: 1825 Sharp Point Drive
;            CITY: Fort Collins
;            STATE: Colorado
;            COUNTRY: USA
;            ZIP: 80525
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: Windows 95
;            SOFTWARE: WordPerfect for Windows, Version 7.0
;       CURRENT APPLICATION DATA:
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;             APPLICATION NUMBER: US/09/944,277A
;             FILING DATE: 30-Aug-2001
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/285,873
;             FILING DATE: 1999-03-31
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Verser, Carol Talkington
;             REGISTRATION NUMBER: 37,459
;             REFERENCE/DOCKET NUMBER: DI-1
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 970/493-7272
;             TELEFAX: 970/484-9505
;   INFORMATION FOR SEQ ID NO: 12:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 516 nucleotides
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       FEATURE:
;             NAME/KEY:   CDS
;             LOCATION:   1..516
;       SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-944-277A-12

  Query Match             66.7%;  Score 516;  DB 9;  Length 516;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-159;
  Matches  516;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         76 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 60

Qy        136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 120

Qy        196 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 180

Qy        256 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240

Qy        316 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 300

Qy        376 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 360

Qy        436 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 420

Qy        496 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 480

Qy        556 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCT 591
              ||||||||||||||||||||||||||||||||||||
Db        481 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCT 516


RESULT 14
US-10-293-992-3
; Sequence 3, Application US/10293992
; Publication No. US20040033527A1
; GENERAL INFORMATION:
;  APPLICANT: Jardetzky, Theodore S.
;  APPLICANT: Garman, Scott Clayton
;  APPLICANT: Kinet, Jean-Pierre
;  TITLE OF INVENTION: METHODS OF USING A THREE-DIMENSIONAL MODEL OF A Fc EPSILON RECEPT
;  TITLE OF INVENTION:  CHAIN
;  FILE REFERENCE: AL-3-C1-1
;  CURRENT APPLICATION NUMBER: US/10/293,992
;  CURRENT FILING DATE:  2002-11-13
;  PRIOR APPLICATION NUMBER: 09/434,193
;  PRIOR FILING DATE: 1999-11-04
;  PRIOR APPLICATION NUMBER: 60/107,219
;  PRIOR FILING DATE: 1998-11-05
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 516
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(516)
;   OTHER INFORMATION:
US-10-293-992-3

  Query Match             66.7%;  Score 516;  DB 13;  Length 516;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-159;
  Matches  516;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         76 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 60

Qy        136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 120

Qy        196 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 255
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Db        121 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 180

Qy        256 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 315
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Db        181 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 240

Qy        316 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 300

Qy        376 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 360

Qy        436 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 420

Qy        496 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 480

Qy        556 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCT 591
              ||||||||||||||||||||||||||||||||||||
Db        481 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCT 516


RESULT 15
US-09-809-715-3
; Sequence 3, Application US/09809715
; Publication No. US20030003502A1
; GENERAL INFORMATION:
;  APPLICANT: Jardetzky, Theodore S.
;  APPLICANT:  Garman, Scott Clayton
;  APPLICANT:  Wurzburg, Beth A.
;  APPLICANT:  Kinet, Jean-Pierre
```

```
;  TITLE OF INVENTION: THREE-DIMENSIONAL MODEL OF A COMPLEX BETWEEN A Fc
;  TITLE OF INVENTION:  EPSILON RECEPTOR ALPHA CHAIN AND A Fc REGION OF AN IgE
;  TITLE OF INVENTION:  ANTIBODY AND USES THEREOF
;  FILE REFERENCE: AL-8
;  CURRENT APPLICATION NUMBER: US/09/809,715
;  CURRENT FILING DATE:  2001-03-14
;  PRIOR APPLICATION NUMBER: 60/189,853
;  PRIOR FILING DATE: 2000-03-15
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 528
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(528)
US-09-809-715-3

  Query Match            66.6%;  Score 515.2;  DB 10;  Length 528;
  Best Local Similarity  98.5%;  Pred. No. 1.3e-158;
  Matches  520;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy         76 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAAAGGAGAG 60

Qy        136 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 195
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Db         61 AATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAATGGTTC 120

Qy        196 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCAAATTT 180

Qy        256 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTGTGTAC 315
              ||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db        181 GAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTGCTGAGAGTGAACCTGTGTAC 240

Qy        316 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGGAGGGC 300

Qy        376 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTAT 360

Qy        436 TATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAAT 495
              |||||||||||||||||||||||| ||||||||||||||   ||||||||||||||||
Db        361 TATAAGGATGGTGAAGCTCTCAAGTATTGGTATGAGAACCACGCTATCTCCATTACAAAT 420

Qy        496 GCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 555
              ||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCGCAGCTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTAT 480

Qy        556 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAG 603
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Db        481 GAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAG 528


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Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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4: em_estmu:*
5: em_estov:*
6: em_estpl:*
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9: gb_est1:*
10: gb_est2:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	690.8	89.3	810	12	BG542554	BG542554 602572052
	2	608	78.6	834	10	BF679057	BF679057 602153315
	3	559.4	72.3	760	12	BG542157	BG542157 602571381
	4	555.6	71.8	840	12	BG548515	BG548515 602576508
	5	500.6	64.7	846	10	BF678252	BF678252 602086161
c	6	475.4	61.4	768	13	BQ573778	BQ573778 UI-H-EZ0-
c	7	417	53.9	707	14	CA448745	CA448745 UI-H-EI0-
c	8	411.6	53.2	712	14	CA419024	CA419024 UI-H-EZ1-
	9	406.4	52.5	818	10	BF677190	BF677190 602087255
c	10	367.6	47.5	669	10	AW612525	AW612525 hh03f07.x
	11	337.4	43.6	660	14	CF362072	CF362072 828457 MA
c	12	326.4	42.2	615	12	BM991911	BM991911 UI-H-DF1-
	13	308.4	39.8	488	13	BX110472	BX110472 BX110472
	14	272.6	35.2	652	13	BY752906	BY752906 BY752906
c	15	254	32.8	570	9	AI676114	AI676114 wc05e12.x
c	16	250	32.3	651	14	CF363368	CF363368 831220 MA
c	17	244.2	31.6	540	9	AI685796	AI685796 tu20g08.x
	18	225.4	29.1	641	14	CB429248	CB429248 605052 MA
	19	222.8	28.8	394	10	AW357271	AW357271 40240 MAR
	20	218.8	28.3	422	10	BF603113	BF603113 268539 MA
c	21	186	24.0	479	10	BF593204	BF593204 7o50c04.x
c	22	184	23.8	478	12	BQ005218	BQ005218 UI-H-EI1-
c	23	180.4	23.3	757	14	CA508723	CA508723 UI-R-FS0-
	24	175.8	22.7	403	14	CB768694	CB768694 AMGNNUC:S
	25	174.4	22.5	1201	9	AL514096	AL514096 AL514096
c	26	173	22.4	446	9	AI676097	AI676097 wc05c12.x
	27	172.4	22.3	429	13	BY228345	BY228345 BY228345
	28	169.8	21.9	848	14	CB958187	CB958187 AGENCOURT
	29	169.4	21.9	1033	9	AL549464	AL549464 AL549464
	30	169.4	21.9	1201	9	AL531122	AL531122 AL531122
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	32	167.8	21.7	1201	13	BX399366	BX399366 BX399366
	33	164.8	21.3	528	14	CB152997	CB152997 K-EST0210
	34	163.8	21.2	823	12	BI768140	BI768140 603056571
	35	163	21.1	1201	13	BX402696	BX402696 BX402696
	36	162.6	21.0	403	13	BY228552	BY228552 BY228552
	37	162.6	21.0	404	13	BY227642	BY227642 BY227642
	38	162.6	21.0	1201	9	AL558081	AL558081 AL558081
	39	162.2	21.0	664	14	CB555672	CB555672 MMSP0057_
	40	162.2	21.0	987	13	BX345202	BX345202 BX345202
	41	161.8	20.9	373	13	BY041924	BY041924 BY041924
	42	161.2	20.8	852	12	BI821954	BI821954 603039767
	43	160	20.7	221	14	CD696486	CD696486 EST13009
	44	158.4	20.5	551	12	BM364531	BM364531 BS3200020
	45	155.6	20.1	571	14	CD693938	CD693938 EST10461

ALIGNMENTS

RESULT 1
BG542554
LOCUS BG542554 810 bp mRNA linear EST 03-APR-2001
DEFINITION 602572052F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4696381 5', mRNA sequence.
ACCESSION BG542554
VERSION BG542554.1 GI:13534787
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 810)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1523 row: h column: 14
High quality sequence stop: 667.

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FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4696381"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_77"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             89.3%;  Score 690.8;  DB 12;  Length 810;
  Best Local Similarity   97.0%;  Pred. No. 4.5e-196;
  Matches  747;  Conservative    0;  Mismatches   17;  Indels    6;  Gaps    4;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 90

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 150

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 210

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 270

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 330

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 390

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 450

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 510

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 570

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600
              |||||||||||||||||||||| |||||||||||||||| ||||||||||||||||||||
Db        571 TGGCAGCTGGACTATGAGTCTGAGGCCCTCAACATTACTGT-ATAAAAGCTCCGCGTGAC 629

Qy        601 AAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACAC- 659
              |||||||||||| |||||||||||||||||||||||||||||||||| ||||||||||| |
Db        630 AAGTACTGGCTACCAATTTTTATCCCATTGTTGGTGGTGATTCTGTTGGCTGTGGACACC 689

Qy        660 -AGGATTATTTATCT-CAACTCAGCAGCAGGTCACATTTCTC--TTGAAGATTAAGAGAA 715
               |||||||||||||| |||||||||||||||||||||||||   |||| |||||  ||||
Db        690 AGGGATTATTTATCTCCAACTCAGCAGCAGGTCACATTTCTCCTTTGACGATTAGAAGAA 749

Qy        716 CCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAA 765
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Db        750 CCCGGAAAGGGCTCAGACTCCTGAACCCAATTCCTAAGACAAACCCAAAA 799


RESULT 2
BF679057
LOCUS       BF679057                834 bp    mRNA    linear   EST 21-DEC-2000
DEFINITION  602153315F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294467 5',
            mRNA sequence.
ACCESSION   BF679057
VERSION     BF679057.1  GI:11952952
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 834)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONETECH Laboratories, Inc.
            cDNA Library Preparation: CLONETECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1143  row: n  column: 04
            High quality sequence stop: 621.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4294467"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_83"
                     /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); 5' and 3' adaptors were used in cloning
                     as follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3'
                     and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.4
                     kb (range 0.5-4.0 kb).  14/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA)."
ORIGIN

  Query Match             78.6%;  Score 608;  DB 10;  Length 834;
  Best Local Similarity   95.8%;  Pred. No. 3.7e-171;
  Matches  657;  Conservative    0;  Mismatches   25;  Indels    4;  Gaps    3;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 90

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 150

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
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Db        151 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 210

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
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Db        211 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 270

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
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Db        271 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 330

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360

Db        331 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 390

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420

Db        391 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 450

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480

Db        451 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAA- 509

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540

Db        510 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 569

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAG 600

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Qy        601 AAGTACTGGCTACAATTTTTTATCCCATT--GTTGGTGGTGATTCTGTTTGCTGTGGACA 658

Db        629 AAGTACTGGCTACAAATTTTTATCCCAATGGGTGGCGGTGAATTCTGGTTGGCGGTGGAC 688

Qy        659 CAGGATTATTTATCTCAACTCAGCAG 684

Db        689 CACGGCTTATTATCCTCACTCAGCGG 714
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RESULT 3
BG542157
LOCUS       BG542157                760 bp    mRNA    linear   EST 03-APR-2001
DEFINITION  602571381F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4695476 5',
            mRNA sequence.
ACCESSION   BG542157
VERSION     BG542157.1  GI:13534390
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 760)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1521  row: b  column: 21
            High quality sequence stop: 751.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_77"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN
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  Query Match             72.3%;  Score 559.4;  DB 12;  Length 760;
  Best Local Similarity   98.5%;  Pred. No. 1.5e-156;
  Matches  596;  Conservative    0;  Mismatches    6;  Indels    3;  Gaps    3;

Qy        167 TCTTTGAAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATT 226

Db         98 TGTTAGCAGTCAGTTCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATT 157

Qy        227 CAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACC 286

Db        158 CAAGTTTGAATATTGTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACC 217

Qy        287 AACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTC 346

Db        218 AACAAGTTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTC 277

Qy        347 AGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGA 406

Db        278 AGGCCTCTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGA 337

Qy        407 GGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGT 466

Db        338 GGAACTGGGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGT 397

Qy        467 ATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACT 526

Db        398 ATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACT 457

Qy        527 GTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAA 586

Db        458 GTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAA 517

Qy        587 AAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGT 646

Db        518 AAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTG- 576

Qy        647 TTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGA 706

Db        577 TTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGA 636

Qy        707 TTAAGAGAACCAGGAAA-GGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAA 765

Db        637 TTAAGAGAACCAGGAAAGGGCTTCAGACTTCTGAACCCA-ATCCTAAGCCAAAACCGAAA 695

Qy        766 AACAA 770

Db        696 AAAAA 700
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RESULT 4
BG548515
LOCUS       BG548515                840 bp    mRNA    linear   EST 04-APR-2001
DEFINITION  602576508F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4704624 5',
            mRNA sequence.
ACCESSION   BG548515
VERSION     BG548515.1  GI:13547180
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 840)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
```

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          Tissue Procurement: CLONTECH Laboratories, Inc.
           cDNA Library Preparation: CLONTECH Laboratories, Inc.
           cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
           DNA Sequencing by: Incyte Genomics, Inc.
           Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLCM1544  row: p  column: 01
          High quality sequence stop: 590.
FEATURES             Location/Qualifiers
     source          1. .840
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4704624"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_77"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             71.8%;  Score 555.6;  DB 12;  Length 840;
  Best Local Similarity   88.3%;  Pred. No. 2.1e-155;
  Matches  701;  Conservative    0;  Mismatches   69;  Indels   24;  Gaps    8;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         31 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 90

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 150

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        151 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 210

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        211 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 270

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 330

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 390

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 450

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              ||||||||||||||||||||||||||||||||||||||||||| |||||||| |  ||
Db        451 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGTTATGAGAAACCAAAA 510

Qy        481 ATCTCCATTACAAAT--GCCACAGTTGAAGACAGTGGAACCTAC-TACTGTACGGGCAAA 537
              |||||||||| |||   |  ||||||||||||||||||||| ||||||||||||||||
Db        511 ATCTCCATTACCAATTGCCACAGTTTGAAGACAGTGGAACCTACTTACTGTACGGGCAAA 570

Qy        538 GTGTGGCAGCTGGAC---------TATGAGTCTGAGCCCCTCAACATTACTGTAA----T 584
              |||||||||||||||         | |||       |  |  |   |||||| |
Db        571 GTGTGGCAGCTGGACCTATGAAGTTCTGAAGGCCCCCTTCAAACATTTACTGTTAATTTA 630

Qy        585 AAAAGCTCCGCGT---GAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGAT 641
              ||| |||||| ||   || |     ||||||||||||| ||  |||||| ||| | |||
Db        631 AAATGCTCCGAGTGAAGAAAGTACTTGGCTACAATTTTATAATCCATTGGTGGGGCTGAA 690

Qy        642 T--CTGTTTGCTGTGGACACAGGA-TTATTTATCTCAACTCAGCA--GCAGGTCACATTT 696
              |  |||||||||||| || | ||| ||||||||||||||||||||   |||||| |||||
Db        691 TCCCTGTTTGCTGTGCACCCCGGATTTATTTATCTCAACTCAGCAAGCCAGGTCCCATTT 750

Qy        697 CTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCA 756
              ||||||||   | ||  ||||  | || | |||||| || ||||||||  |||  || ||
Db        751 CTCTTGAAAGATTAGGAAACCCAGGAAAGGTTCAGAATTTTGAACCCAATTCCATAGGCA 810

Qy        757 AACCCCAAAAACAA 770
              || ||| |||||||
Db        811 AAACCCCAAAACAA 824


RESULT 5
BF678252
LOCUS       BF678252                846 bp    mRNA    linear   EST 21-DEC-2000
DEFINITION  602086161F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4250222 5',
            mRNA sequence.
ACCESSION   BF678252
VERSION     BF678252.1  GI:11952147
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 846)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONETECH Laboratories, Inc.
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1071  row: j  column: 15
            High quality sequence stop: 609.
FEATURES             Location/Qualifiers
     source          1. .846
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4250222"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_83"
                     /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); 5' and 3' adaptors were used in cloning
                     as follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3'
                     and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.4
                     kb (range 0.5-4.0 kb).  14/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA)."
ORIGIN

  Query Match             64.7%;  Score 500.6;  DB 10;  Length 846;
  Best Local Similarity   92.8%;  Pred. No. 7.6e-139;
  Matches  636;  Conservative    0;  Mismatches   34;  Indels   15;  Gaps   10;

Qy         12 CATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTT 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 CATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCAGATGGCGTGTT 95
```

```
Qy         72 AGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAA-AG 130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db         96 AGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAATATTTAACAG 155

Qy        131 GAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAAT 190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 GAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGTTCCACCAAAT 215

Qy        191 GGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATTGTGAATGCCA 250
              |||||||||||||||||||||||||||||||||||||||||    |   ||||||||||
Db        216 GGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTT--GAATATGTGAATGCCA 273

Qy        251 AATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTG 310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 AATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAGAGTGAACCTG 333

Qy        311 TGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGG 370
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        334 TGTACCTGGAAGTCTTCAGTGACT-GCTGCTCCTTCAGGCCTCTGCTGAGGTGGTGATGG 392

Qy        371 AGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGA 430
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        393 AGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACT-GGATGTGTACAAGGTGA 451

Qy        431 TCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTA 490
              |||||||||||||||||||||||||||||||| ||||||||||||| ||||||||||
Db        452 TCTATTATAAGGATGGTGAAGCTCTCAAGTACT-GTATGAGAACCACAA-ATCTCCATTA 509

Qy        491 CAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGG 550
              |||||||||||| |||||||||||||||||||||||||||||  |||||||||||||| |
Db        510 CAAATGCCACAG-TGAAGACAGTGGAACCTACTACTGTACGGGGCAAGTGTGGCAGCT-G 567

Qy        551 ACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGC 610
              |||||||||||||||||||||||||| || |||||||||||||||| |     | ||||||
Db        568 ACTATGAGTCTGAGCCCCTCAAAATAACTGTAATAAAAGCTCGGGTGAGAAGGTACTGCT 627

Qy        611 TACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTA 670
                || |||||||||||||||| || | |     | | ||    |||||||||||||| |||
Db        628 ACCACTTTTTTATCCCATTGTGGGGGAT-----TCTGTGGCTGGGACACAGGATTA-TTA 681

Qy        671 TCTCAACTCAGCAGCAGGTCACATT 695
              |||||||||||||  ||| ||||
Db        682 TCTCAACTCAGCAGGCAGTCCCATT 706
```

RESULT 6
BQ573778/c

```
LOCUS       BQ573778                768 bp    mRNA    linear   EST 19-JUN-2002
DEFINITION  UI-H-EZ0-bav-l-04-0-UI.s1 NCI_CGAP_Ch1 Homo sapiens cDNA clone
            UI-H-EZ0-bav-l-04-0-UI 3', mRNA sequence.
ACCESSION   BQ573778
VERSION     BQ573778.1  GI:21477095
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 768)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
            Orthoapedics
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 1-41, >AT_rich#Low_complexity (matched compliment)
            93-129, >LINE2 (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .768
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-EZ0-bav-l-04-0-UI"
                     /tissue_type="Chondrosarcoma Grade II"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_Ch1"
                     /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                     with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_Ch1 is a cDNA library containing the following
                     tissue(s): Chondrosarcoma Grade II. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     TGATCACGCT.
                     TAG_TISSUE=grade-2-chondrosarcoma
                     TAG_LIB=UI-H-EZ0
                     TAG_SEQ=ATCTAATATG"
ORIGIN
```

```
  Query Match             61.4%;  Score 475.4;  DB 13;  Length 768;
  Best Local Similarity   99.6%;  Pred. No. 2.7e-131;
  Matches  476;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        297 TGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGC 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        768 TGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGC 709

Qy        357 TGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGA 416
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        708 TGAGGTGGTGATGGAGGNCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGA 649

Qy        417 TGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCA 476
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        648 TGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCA 589

Qy        477 CAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAA 536
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        588 CAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAA 529

Qy        537 AGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCG 596
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        528 AGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCG 469

Qy        597 TGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGA 656
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        468 TGAGAAGTACTGGCTACAATTTTTTATCCCATTCTTGGTGGTGATTCTGTTTGCTGTGGA 409

Qy        657 CACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAAC 716
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        408 CACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAAC 349

Qy        717 CAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        348 CAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 291
```

RESULT 7
CA448745/c

```
LOCUS       CA448745                707 bp    mRNA    linear   EST 08-NOV-2002
DEFINITION  UI-H-EI0-ayo-p-24-0-UI.s1 NCI_CGAP_EI0 Homo sapiens cDNA clone
```

```
            UI-H-EI0-ayo-p-24-0-UI 3', mRNA sequence.
ACCESSION   CA448745
VERSION     CA448745.1  GI:24813165
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 707)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 93-129, >LINE2 (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .707
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-EI0-ayo-p-24-0-UI"
                     /tissue_type="Chondrosarcoma"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_EI0"
                     /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                     with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_EI0 is a cDNA library containing the following
                     tissue(s): Chondrosarcoma. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is ACACTTGCAC.
                     TAG_TISSUE=chondrosarcoma
                     TAG_LIB=UI-H-EI0
                     TAG_SEQ=ACACTTGCAC"
ORIGIN
```

Query Match 53.9%; Score 417; DB 14; Length 707;
Best Local Similarity 100.0%; Pred. No. 9.6e-114;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy        358 GAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGAT 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        707 GAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGAT 648

Qy        418 GTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAC 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        647 GTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCAC 588

Qy        478 AACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAA 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        587 AACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAA 528

Qy        538 GTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGT 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        527 GTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGT 468
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Qy        598 GAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGAC 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        467 GAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGAC 408

Qy        658 ACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACC 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        407 ACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACC 348

Qy        718 AGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        347 AGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 291
```

```
RESULT 8
CA419024/c
LOCUS       CA419024                712 bp    mRNA    linear   EST 07-NOV-2002
DEFINITION  UI-H-EZ1-bbj-e-19-0-UI.s1 NCI_CGAP_Ch2 Homo sapiens cDNA clone
            UI-H-EZ1-bbj-e-19-0-UI 3', mRNA sequence.
ACCESSION   CA419024
VERSION     CA419024.1  GI:24781675
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 712)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
            Orthoapedics
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 1-42, >(TAAAA)n#Simple_repeat (matched compliment)
            94-130, >LINE2 (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .712
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-EZ1-bbj-e-19-0-UI"
                     /tissue_type="Chondrosarcoma Grade II"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_Ch2"
                     /note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
                     with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_Ch2 is a normalized cDNA library containing the
                     following tissue(s): Chondrosarcoma Grade II. The library
                     was constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     TGATCACGCT.
                     TAG_TISSUE=grade-2-chondrosarcoma
                     TAG_LIB=UI-H-EZ1
                     TAG_SEQ=ATCTAATATG"
ORIGIN
```

```
  Query Match          53.2%;  Score 411.6;  DB 14;  Length 712;
  Best Local Similarity  98.3%;  Pred. No. 4e-112;
  Matches  414;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy        354 TGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTG 413
              ||||||||||||||||||| |||||||||||||||||||||||||  ||||||||||
Db        712 TGCTGAGGTGGTGATGGAGGNCCAGCCCCTCTTCCTCAGGTGCCATGTNTGGAGGAACTG 653

Qy        414 GGATGTGTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAA 473
              |||||||||||||||||||    | ||||||||||||||||||||||||||||||||||
Db        652 GGATGTGTACAAGGTGATCTATATAANGGATGGTGAAGCTCTCAAGTACTGGTATGAGAA 593

Qy        474 CCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGG 533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 CCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGG 533

Qy        534 CAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCC 593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 CAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCC 473

Qy        594 GCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGT 653
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 GCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGTTTGCTGT 413

Qy        654 GGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAG 713
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 GGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAAGATTAAGAG 353

Qy        714 AACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTG 773
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 AACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAAAAACAACTG 293

Qy        774 A 774
              |
Db        292 A 292
```

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RESULT 9
BF677190
LOCUS       BF677190                818 bp    mRNA    linear   EST 21-DEC-2000
DEFINITION  602087255F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4251469 5',
            mRNA sequence.
ACCESSION   BF677190
VERSION     BF677190.1  GI:11951085
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 818)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONETECH Laboratories, Inc.
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1074  row: n  column: 14
            High quality sequence stop: 616.
FEATURES             Location/Qualifiers
     source          1. .818
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4251469"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_83"
                     /note="Organ: prostate; Vector: pDNR-LIB (Clontech);
                     Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI
                     (ggccattatggcc); 5' and 3' adaptors were used in cloning
                     as follows: 5' adaptor sequence:  5'-CACGGCCATTATGGCC-3'
                     and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.4
                     kb (range 0.5-4.0 kb).  14/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA)."
ORIGIN
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  Query Match          52.5%;  Score 406.4;  DB 10;  Length 818;
  Best Local Similarity  83.3%;  Pred. No. 1.6e-110;
  Matches  583;  Conservative    0;  Mismatches  101;  Indels   16;  Gaps   10;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              |||||||||||| || |  |||         ||||||||||||||||||||||||||||
Db         35 ATGGCTCCTGCCAAGGGAATCCCCTACTCTATGTGTGTAGCCTTACTGTTCTTCGCTCCA 94

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         95 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 154

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTT-TGAAGTCAG 179
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        155 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTGTGAAGTCAG 214

Qy        180 TTCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATA- 238
              |||||||||||||||||||||||||||||||||||||||||||||  |  |||   |
Db        215 TTCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTTCAAGTTGTGAAC 274

Qy        239 ---TTGTGAATGCCAAAT--TTGAAGACAGTGGAGAAT-ACAAATGTCAGCACCAACAAG 292
                  |||||||||||||  |  |  ||||||  ||||  ||||||||||||||||||||
Db        275 TACTGGTGAATGCCAAATTGTGAAGACCAGTGGCGAATAACAAATGTCAGCACCAACAAG 334

Qy        293 TTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCT 352
              ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        335 TTAATGAGAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTTGCTGCTCCTTCAGGCCT 394

Qy        353 CTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACT 412
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        395 CTGCTGAGGTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGACAC 454

Qy        413 GGGATGTGTAC-AAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAG 471
              |||||||||| |||||||||||||||||||||||||||||||||||||||| |||||||
Db        455 TGGATGTGTACAAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACT-GTATGAG 513

Qy        472 AACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACC---TACTACTGT 528
              ||||| || || |||||||||||||||||||| |||||||| || | |   |||
Db        514 AACCA-AAAATTTCCATTACAAATGCCACAGTGGAAGACAGGGGGAACCTAACTACTTGT 572

Qy        529 ACGGGCAAA-GTGTGGCAGCTGGACTA-TGAGTCTGAGCCCCTCAACATTACTGTAATAA 586
              ||||||||| |||||||| ||||||| |||||||     |||||||||||| |||||| |
Db        573 ACGGGCAAAGGTGTGGCAAGTGGACTATTGAGTCTTGAGCCCTCAACATTAGTGTAATTA 632

Qy        587 AAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCTGT 646
              |||   |  ||| ||   | |  |   |   | ||          | |  ||   ||||
Db        633 AAGGCTCCGGTGGGAGAAAGTTACGGTACAATATTTAATACCATTGGTGGGGTGATCTGG 692

Qy        647 TTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCA 686
              ||| |||||| |  |||||||  |   | | ||  |||
Db        693 TTGGTGTGGAAAAGGGATTATTATTTCAATCGAAGGGGCA 732
```

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RESULT 10
AW612525/c
LOCUS       AW612525                669 bp    mRNA    linear   EST 23-MAR-2000
DEFINITION  hh03f07.x1 NCI_CGAP_Kid11 Homo sapiens cDNA clone IMAGE:2954053 3'
            similar to gb:X06948 HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR
            ALPHA-SUBUNIT (HUMAN);, mRNA sequence.
ACCESSION   AW612525
VERSION     AW612525.1  GI:7317711
```

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KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            image.llnl.gov/image/html/iresources.shtml
            Seq primer: -40UP from Gibco
            High quality sequence stop: 438.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2954053"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Kid11"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Plasmid DNA from the normalized library NCI_CGAP_Kid3 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1322376-1323911, 1456007-1456775, and
                     1500552-1502855). Subtraction by Bento Soares and M.
                     Fatima Bonaldo.  "
ORIGIN
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  Query Match           47.5%;  Score 367.6;  DB 10;  Length 669;
  Best Local Similarity  97.2%;  Pred. No. 6.7e-99;
  Matches  384;  Conservative    0;  Mismatches   10;  Indels    1;  Gaps    1;

Qy        381 CCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTGTACAAGGTGATCTATTATAA 440
              ||||||| |||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        669 CCTCTTCTCCAGGTGCCATGGTTGCAGGAACTGGGATGTGTACAAGGTGATCTATTATAA 610

Qy        441 GGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCAC 500
              |||||||||||||||||||| |||||||||||||||||||||||||||| |||||||
Db        609 GGATGGTGAAGCTCTCAAGTGCTGGTATGAGAACCACAACATCTCCATTACATATGCCAC 550

Qy        501 AGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTC 560
              |||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Db        549 AGTTGAAGACAGTGGAACCTACTACTGTACGGGCACAGTGTGGCAGCTGGAATATGAGTC 490

Qy        561 TGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAA-TTTT 619
              |||||||||||||||||||||||| ||||| |||||||||||||||||||| ||||
Db        489 TGAGCCCCTCAACATTACTGTAATAANAGCTCTGCGTGAGAAGTACTGGCTACAATTTTT 430

Qy        620 TTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTC 679
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TTATCCCATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTC 370

Qy        680 AGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGA 739
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 AGCAGCAGGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGA 310

Qy        740 ACCCACATCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||| |||||||||||||||||||||||
Db        309 ACCCACATCTTAAGCCAAACCCCAAAAACAACTGA 275
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RESULT 11
CF362072
LOCUS       CF362072                660 bp    mRNA    linear   EST 25-AUG-2003
DEFINITION  828457 MARC 3PIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION   CF362072
VERSION     CF362072.1  GI:34161364
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Fox,J.,
            Wise,T.A., Nonneman,D.J., Wray,J.E. and Keele,J.W.
  TITLE     A second set of porcine ESTs from a pooled-tissue normalized
            library
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: SRG8018  row: L  column: 4
            Seq primer: GTAATACGACTCACTATAGGG.
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /tissue_type="pooled"
                     /lab_host="DH10B"
                     /clone_lib="MARC 3PIG"
                     /note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
                     Library made with RNA pooled from multiple tissues
                     including brain, liver, muscle, placenta/endometrium,
                     ovary, testes, and bone marrow."
ORIGIN
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  Query Match           43.6%;  Score 337.4;  DB 14;  Length 660;
  Best Local Similarity  71.6%;  Pred. No. 8.1e-90;
  Matches  462;  Conservative    0;  Mismatches  171;  Indels   12;  Gaps    1;

Qy          1 ATGGCTCCTGCCATGGAATCCCCTACTCTACTGTGTGTAGCCTTACTGTTCTTCGCTCCA 60
              ||| || || |||| | | |||| | || || || |||| | ||| ||||| |||||
Db         16 ATGTCTACTCCCATAGGAGTCCCTGCCCTGCTATGGATAGCTCTGCTGCTCTTCTCTCCA 75

Qy         61 GATGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGA 120
              |||||| ||  |||||||   ||| || || |||| |||||||| || |||||||||| ||
Db         76 GATGGCATGGCAGCAGTCATCCAGGAATCTCAGGTGTCCTTGAATCCCCCATGGAATCGA 135

Qy        121 ATATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGTCAGT 180
              ||||||| |||||||||||||||||| ||||||| ||||||| ||  | |||||
Db        136 ATATTTAGAGGAGAGAATGTGACTCTCACATGTATTGGGAACGATGCCCTTGAAAATTAC 195

Qy        181 TCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATATT 240
              ||||||| |||   |||||   ||   ||  |||| || || ||| |||| | |  ||
Db        196 CCCACCAATTGGACACACAACAACAAAACTTTGGAAGTGAAAACTTCGAGTTGGGACCTT 255

Qy        241 GTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGAG 300
              ||||||| |||  || ||||| ||  |||||| ||| ||   | || |  |||    |
Db        256 AAGAATGCAAAACCTGGGGACAGCGGCAAATACAGATGCCAAAGCAAAGACTTTACAATG 315

Qy        301 AGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGAG 360
              |||||||||||| |||| |||||| |||||||||||||||||||||| ||||||   |
Db        316 AGTGAACCTGTGCACCTAGAAGTCATCAGTGACTGGCTGCTCCTTCAGACCTCTGTCCCG 375

Qy        361 GTGGTGATGGAGGGCCAGCCCCTCTTCCTCAGGTGCCATGGTTGGAGGAACTGGGATGTG 420
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                ||||||| ||| |||||| || || |||||| ||| || || |||| |||    | ||||
Db        376 GTGGTGAGGGAAGGCCAGTCCTTCCTCCTCATGTGTCACGGCTGGAAGAATCTGAATGTC 435

Qy        421 TACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAAC 480
              || |||||||||||| || ||||||||  |||| ||||||||||||||||||||||||||
Db        436 TATAAGGTGATCTACTACAAGGATGGCAAAGCCCTCAAGTACTGGTATGAGAACCACAAC 495

Qy        481 ATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGTG 540
              |||||||||| ||||||| |   |||||||||||  | || |  || ||||||| | |
Db        496 CTCTCCATTACCAATGCCAAAAGAGAAGACAGTGGCTCTTATTGGTGCACGGGCATAATT 555

Qy        541 TGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCTCCGCGT--- 597
              | |     |  | |||     | |||| ||||||  ||  || || | | | |
Db        556 CAAAAAATACCAAAAAACTCTACTACTCTCACCATTACCATACAAACAGATTCCCCTTCA 615

Qy        598 ---------GAGAAGTACTGGCTACAATTTTTTATCCCATTGTTG 633
                      |  | ||||||||||||  ||  |||||||||||||
Db        616 GTTCCCTCGAACTATTACTGGCTACAGCTTCATATCCCATTGTTG 660


RESULT 12
BM991911/c
LOCUS       BM991911                615 bp    mRNA    linear   EST 17-JUN-2002
DEFINITION  UI-H-DF1-auk-l-12-0-UI.s1 NCI_CGAP_DF1 Homo sapiens cDNA clone
            IMAGE:5870747 3', mRNA sequence.
ACCESSION   BM991911
VERSION     BM991911.1  GI:19711300
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 615)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jose Mercuende
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
             The following repetitive elements were found in this cDNA
            sequence: 90-126, >LINE2 (matched compliment)
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .615
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5870747"
                     /tissue_type="Subchondral Bone"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_DF1"
                     /note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_DF1 is a normalized cDNA library containing the
                     following tissue(s): Subchondral Bone. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GTTAAGCGTC.
                     TAG_TISSUE=subchondral bone
                     TAG_LIB=UI-H-DF1
                     TAG_SEQ=GTTAAGCGTC"
ORIGIN

  Query Match           42.2%;  Score 326.4;  DB 12;  Length 615;
  Best Local Similarity   99.7%;  Pred. No. 1.6e-86;
  Matches  327;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        447 TGAAGCTCTCAAGTACTGGTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGA 506
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        615 TGAAGCTCTCAAGTACTGGTGTGAGAACCACAACATCTCCATTACAAATGCCACAGTTGA 556

Qy        507 AGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCC 566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        555 AGACAGTGGAACCTACTACTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCC 496

Qy        567 CCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCC 626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        495 CCTCAACATTACTGTAATAAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCC 436

Qy        627 ATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCA 686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        435 ATTGTTGGTGGTGATTCTGTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCA 376

Qy        687 GGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACA 746
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        375 GGTCACATTTCTCTTGAAGATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACA 316

Qy        747 TCCTAAGCCAAACCCCAAAAACAACTGA 774
              ||||||||||||||||||||||||||||
Db        315 TCCTAAGCCAAACCCCAAAAACAACTGA 288


RESULT 13
BX110472
LOCUS       BX110472                488 bp    mRNA    linear   EST 07-FEB-2003
DEFINITION  BX110472 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGp998B235736 ;
            IMAGE:2314294, mRNA sequence.
ACCESSION   BX110472
VERSION     BX110472.1  GI:27836404
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 488)
  AUTHORS   Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
            Radelof,U., Schneider,D. and Korn,B.
  TITLE     Human UnigeneSet - RZPD3
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998B235736.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Human UnigeneSet - RZPD3 (RZPDLIB No.972)
            http://www.rzpd.de/CloneCards/cgi-
            bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .488
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGp998B235736 ; IMAGE:2314294"
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/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Pr28"
/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Pr22 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 39.8%; Score 308.4; DB 13; Length 488;
Best Local Similarity 99.7%; Pred. No. 3.6e-81;
Matches 309; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy        465 GTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTA 524
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Qy        525 CTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCCTCAACATTACTGTAAT 584
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Qy        585 AAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCT 644
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Db        121 AAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCT 180

Qy        645 GTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAA 704
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAA 240

Qy        705 GATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAA 764
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Qy        765 AAACAACTGA 774
              ||||||||||
Db        301 AAACAACTGA 310
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RESULT 14
BY752906
LOCUS BY752906 652 bp mRNA linear EST 17-DEC-2002
DEFINITION BY752906 RIKEN full-length enriched, adult inner ear Mus musculus cDNA clone F930034C11 5', mRNA sequence.
ACCESSION BY752906
VERSION BY752906.1 GI:27184082
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 652)
AUTHORS Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Semple,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
MEDLINE 22354683
PUBMED 12466851
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Tissues were provided by Kirk W. Beisel (Boys Town National Research Hospital 555 North 30th Street Omaha,NE 68131 USA) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
FEATURES Location/Qualifiers
source 1. .652
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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ORIGIN

Query Match 35.2%; Score 272.6; DB 13; Length 652;
Best Local Similarity 68.6%; Pred. No. 2.5e-70;
Matches 406; Conservative 0; Mismatches 180; Indels 6; Gaps 2;

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Qy         63 TGGCGTGTTAGCAGTCCCTCAGAAACCTAAGGTCTCCTTGAACCCTCCATGGAATAGAAT 122
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Db         89 TGTCATTCTGACAGCCACTGAGAAATCTGTACTGACCTTGGACCCACCATGGATTAGAAT 148

Qy        123 ATTTAAAGGAGAGAATGTGACTCTTACATGTAATGGGAACAATTTCTTTGAAGT---CAG 179
              |||||  |||||||||  |||||  |||  | ||  ||||||||||  | ||  ||  |   |
Db        149 ATTTACAGGAGAGAAAGTGACCCTTTCCTGCTATGGGAACAATCACCTTCAAATGAACTC 208

Qy        180 TTCCACCAAATGGTTCCACAATGGCAGCCTTTCAGAAGAGACAAATTCAAGTTTGAATAT 239
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Qy        240 TGTGAATGCCAAATTTGAAGACAGTGGAGAATACAAATGTCAGCACCAACAAGTTAATGA 299
              |||||  |||||    ||  ||||||||||||  ||||||  |||||||  | |||  | |   | |
Db        269 TGTGAGTGCCACCGTTCAAGACAGTGGAAAATACATATGTCAGAAGCAAGGATTGTTTAA 328

Qy        300 GAGTGAACCTGTGTACCTGGAAGTCTTCAGTGACTGGCTGCTCCTTCAGGCCTCTGCTGA 359
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Qy        420 GTACAAGGTGATCTATTATAAGGATGGTGAAGCTCTCAAGTACTGGTATGAGAACCACAA 479
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Qy        480 CATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTACTGTACGGGCAAAGT 539
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Db        506 CGTCTCCATTAGAGAGGCCACACTGAATGACAGTGGCACCTACCACTGNCAGGGCTATCT 565

Qy        540 GTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAATAAAAGCT 591
                |||||  |||| |||||  |||||      |||  |||  |||||  ||||||||
Db        566 TAGGCAGGTGGAATATGAATCTGACAAATTCAGAATTGCTGTAGTAAAAGCT 617


RESULT 15
AI676114/c
LOCUS       AI676114                570 bp    mRNA    linear   EST 17-DEC-1999
DEFINITION  wc05e12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314318 3'
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            ALPHA-SUBUNIT (HUMAN);, mRNA sequence.
ACCESSION   AI676114
VERSION     AI676114.1  GI:4876594
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 570)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
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                     /clone_lib="NCI_CGAP_Pr28"
                     /note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
                     with a modified polylinker; Plasmid DNA from the
                     normalized library NCI_CGAP_Pr22 was prepared, and ss
                     circles were made in vitro. Following HAP purification,
                     this DNA was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from a pool
                     of 5,000 clones made from the same library (cloneIDs
                     985608-986759, 1101192-1101959, and 1217928-1220615).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
ORIGIN

  Query Match           32.8%;  Score 254;  DB 9;  Length 570;
  Best Local Similarity   88.7%;  Pred. No. 9.1e-65;
  Matches  275;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy        465 GTATGAGAACCACAACATCTCCATTACAAATGCCACAGTTGAAGACAGTGGAACCTACTA 524
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Db        570 GTATGAGAATCGCATCTGTGCCATAGCGAATGCCGAGGTGATAGACAGTAGGGCCTATTG 511

Qy        525 CTGTACGGGCAAAGTGTGGCAGCTGGACTATGAGTCTGAGCCCCTCAACATTACTGTAAT 584
              |||| ||||||||||||||||||||| |||| ||||||||||    ||||||  ||||||
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Qy        585 AAAAGCTCCGCGTGAGAAGTACTGGCTACAATTTTTTATCCCATTGTTGGTGGTGATTCT 644
              |||||||||||||  || || |||||| |||||||||||||||||||||||||||||||||
Db        450 AAAAGCTCCGCGTCAGGAGGACTGGCAACAATTTTTTATCCCATTGTTGGTGGTGATTCT 391

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Db        390 GTTTGCTGTGGACACAGGATTATTTATCTCAACTCAGCAGCAGGTCACATTTCTCTTGAA 331

Qy        705 GATTAAGAGAACCAGGAAAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAA 764
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Db        330 GATTAAGAGAACCAGGAGAGGCTTCAGACTTCTGAACCCACATCCTAAGCCAAACCCCAA 271

Qy        765 AAACAACTGA 774
              |||||  ||||
Db        270 AAACAGCTGA 261


Search completed: October 10, 2004, 19:44:37
Job time : 2613.69 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: October 6, 2004, 08:59:38 ; Search time 52.4569 Seconds
(without alignments)
1249.617 Million cell updates/sec

Title: US-10-763-400-6
Perfect score: 1264
Sequence: 1 VPQKPKVSLNPPWNRIFKGE.....RTRKGFRLLNPHPKPNPKNN 232

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1264	100.0	232	4	AAB31585	Aab31585 Amino aci
2	1264	100.0	257	1	AAP90385	Aap90385 Alpha sub
3	1264	100.0	257	2	AAR05025	Aar05025 Alpha sub
4	1264	100.0	257	2	AAR14772	Aar14772 Human Fc(
5	1264	100.0	257	2	AAR42336	Aar42336 Human Fce
6	1264	100.0	257	2	AAW24066	Aaw24066 Alpha sub
7	1264	100.0	257	2	AAW61190	Aaw61190 The alpha
8	1264	100.0	257	4	AAB74667	Aab74667 Human imm
9	1264	100.0	257	4	AAB31584	Aab31584 Amino aci
10	1264	100.0	257	5	ABG32801	Abg32801 Human IgE
11	1264	100.0	257	6	ABO01301	Abo01301 Human pro
12	1264	100.0	257	7	ADD48674	Add48674 Human Pro
13	1264	100.0	260	3	AAY96230	Aay96230 Human Fc
14	1259	99.6	257	2	AAW48094	Aaw48094 Human IgE
15	1251	99.0	257	7	ADB85536	Adb85536 Human imm
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19	1002	79.3	183	3	AAY96232	Aay96232 Recombina
20	991	78.4	978	2	AAW48096	Aaw48096 Human ser
21	991	78.4	978	5	ABG32803	Abg32803 Human IgE
22	981.5	77.7	235	2	AAR26064	Aar26064 Human FcE
23	969	76.7	176	3	AAY94210	Aay94210 Human PhF
24	969	76.7	176	4	AAG65597	Aag65597 Amino aci
25	947	74.9	172	2	AAY33185	Aay33185 Human sFc
26	947	74.9	172	3	AAY94211	Aay94211 Human PhF
27	947	74.9	172	4	AAB31587	Aab31587 A Fc epsi
28	947	74.9	197	2	AAR45778	Aar45778 Human dih
29	947	74.9	197	4	AAB31586	Aab31586 A Fc epsi
30	947	74.9	635	4	AAB31594	Aab31594 Fc epsilo
31	947	74.9	660	4	AAB31593	Aab31593 Fc epsilo
32	947	74.9	731	4	AAB31591	Aab31591 Amino aci
33	947	74.9	756	4	AAB31590	Aab31590 Amino aci
34	944	74.7	176	4	AAG65598	Aag65598 Amino aci
35	938	74.2	193	2	AAR89281	Aar89281 IgE high
36	785.5	62.1	236	2	AAY27060	Aay27060 Equine Fc
37	785.5	62.1	255	2	AAY27058	Aay27058 Equine Fc
38	775	61.3	281	2	AAR13867	Aar13867 Hybrid Fc
39	679	53.7	281	2	AAR13870	Aar13870 Hybrid Fc
40	676	53.5	229	2	AAW81114	Aaw81114 Canine Fc
41	676	53.5	253	2	AAW81113	Aaw81113 Canine Fc
42	639	50.6	281	2	AAR13872	Aar13872 Fc(gamma)
43	606	47.9	281	2	AAR13869	Aar13869 Hybrid Fc
44	576.5	45.6	245	1	AAP90386	Aap90386 Alpha sub
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ALIGNMENTS

RESULT 1
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ID AAB31585 standard; protein; 232 AA.
XX
AC AAB31585;
XX
DT 30-APR-2001 (first entry)
XX
DE Amino acid sequence of Fc epsilon receptor alpha-chain mature protein.
XX
KW Fc epsilon receptor; FcepsilonR; immunoglobulin E; IgE; atopic disease;
KW luminescence inducing protein; allergy; hyper IgE syndrome;
KW internal parasite infection; B cell neoplasia.
XX
OS Homo sapiens.
XX
PN WO200104310-A1.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US019070.
XX
PR 13-JUL-1999; 99US-0143612P.
PR 02-MAR-2000; 2000US-0186412P.
XX
PA (HESK-) HESKA CORP.
PA (PROM-) PROMEGA CORP.
XX
PI Weber ER, Wood KV, Hall MP;
XX
DR WPI; 2001-103082/11.
DR N-PSDB; AAF24913.
XX
PT A fusion protein, comprising an Fc epsilon receptor domain and a
PT luminescence inducing protein domain that induces a LP substrate to emit
PT light when contacted with the LP domain, useful for detecting
PT immunoglobulin (Ig) E.
XX
PS Claim 16; Page 62-63; 105pp; English.
XX
CC The present sequence represents a human Fc epsilon receptor (FcepsilonR)
CC alpha-chain mature protein, that binds to immunoglobulin (Ig) E). The
CC FcepsilonR domain is used to produce a fusion protein, which also
CC comprises a luminescence inducing protein domain that induces a substrate
CC to emit light when contacted with the luminescence inducing protein
CC domain. The fusion protein may be used to detect IgE. It may also be used
CC to identify a compound capable of inhibiting FcepsilonR protein activity.
CC IgE antibody production is indicative of diseases such as allergies,

```
CC   atopic disease, hyper IgE syndrome, internal parasite infections and B
CC   cell neoplasia. Detection of IgE production in an animal following
CC   therapy is indicative of the efficacy of the treatment, for example when
CC   using treatments intended to disrupt IgE production
XX
SQ   Sequence 232 AA;

  Query Match           100.0%;  Score 1264;  DB 4;  Length 232;
  Best Local Similarity  100.0%;  Pred. No. 4.5e-93;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60

Qy         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120

Qy        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180
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Db        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180

Qy        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232


RESULT 2
AAP90385
ID   AAP90385 standard; protein; 257 AA.
XX
AC   AAP90385;
XX
DT   24-OCT-2003  (revised)
DT   25-MAR-2003  (revised)
DT   01-NOV-1989  (first entry)
XX
DE   Alpha subunit of human mast cell IgE surface receptor.
XX
KW   Immunoglobulin E receptor alpha subunit; allergies;
KW   non-peptide drug design; human.
XX
OS   Homo sapiens; (Human); mast cell line.
OS   KU812.
XX
PN   WO8905352-A.
XX
PD   15-JUN-1989.
XX
PF   29-NOV-1988;   88WO-US004255.
XX
PR   01-DEC-1987;   87US-00127214.
XX
PA   (HARD ) HARVARD COLLEGE.
PA   (USSH ) NAT INST OF HEALTH.
XX
PI   Leder P,  Benfey P;
XX
DR   WPI; 1989-192698/26.
DR   N-PSDB; AAN90126.
XX
PT   CDNA encoding IGE receptor alpha-sub-unit - used to treat allergies.
XX
PS   Disclosure; Fig 4; 17pp; English.
XX
CC   Immunoglobulin E receptor alpha subunit of human mast cell IgE surface
CC   recptor (see corresp. AAN90126). Used to produce antibodies which can
CC   diagnose IgE receptor levels, measure and treat allergies, and design non
CC   -peptide drugs. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
CC   24-OCT-2003 to standardise OS field)
XX
SQ   Sequence 257 AA;

  Query Match           100.0%;  Score 1264;  DB 1;  Length 257;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-93;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85

Qy         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145

Qy        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205

Qy        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257


RESULT 3
AAR05025
ID   AAR05025 standard; protein; 257 AA.
XX
AC   AAR05025;
XX
DT   02-OCT-1990  (first entry)
XX
DE   Alpha subunit of human high affinity IgE receptor.
XX
KW   high affinity IgE receptor; alpha subunit of IgE receptor; human;
KW   allergic response; ss.
XX
OS   Synthetic.
XX
PN   WO9004640-A.
XX
PD   03-MAY-1990.
XX
PF   18-OCT-1988;   88US-00259065.
XX
PR   18-OCT-1988;   88US-00259065.
XX
PA   (USDC ) US SEC OF COMMERCE.
XX
PI   Kinet JP,  Metzger H;
XX
DR   WPI; 1990-164023/21.
DR   N-PSDB; AAQ04644.
XX
PT   DNA sequences for sub-unit peptide(s) of high affinity IgE receptor - and
PT   derived polypeptides, for therapy and diagnosis of allergies, and studies
PT   of IgE receptor interaction.
XX
PS   Disclosure; Page ?; -pp; English.
XX
CC   The high affinity receptor is a tetrameric complex consisting of 2 gamma
CC   subunits and one each of subunits alpha and beta. It is expressed on mast
CC   cells and is involved in the allergic response. COS-7 cells cotransfected
CC   with cDNA for all 3 intact subunit types (derived from rat basophilic
CC   leukaemia cells) express receptor on their surfaces. Detailed study of
CC   the receptors is now possible. See also AAQ04643 and AAQ04645-6
XX
SQ   Sequence 257 AA;

  Query Match           100.0%;  Score 1264;  DB 2;  Length 257;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-93;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85

Qy         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145

Qy        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205

Qy        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257
```

```
RESULT 4
AAR14772
ID   AAR14772 standard; protein; 257 AA.
XX
AC   AAR14772;
XX
DT   25-MAR-2003  (revised)
DT   17-DEC-2001  (revised)
DT   03-FEB-1992  (first entry)
XX
DE   Human Fc(epsilon)RI alpha subunit.
XX
KW   Immunoglobulin; receptor; high affinity receptor.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /label= signal
FT   Protein         26. .257
FT                   /label= alpha_subunit
FT   Domain          80. .104
FT                   /label= homologous_domain
FT                   /note= "homologous to residues 163-190"
FT   Domain          163. .190
FT                   /label= homologous_domain
FT                   /note= "homologous to residues 80-104"
FT   Region          205. .224
FT                   /label= transmembrane
FT   Region          225. .257
FT                   /label= cytoplasmic
XX
PN   USN7626704-N.
XX
PD   15-OCT-1991.
XX
PF   14-DEC-1990;   90US-00626704.
XX
PR   14-DEC-1990;   90US-00626704.
XX
PA   (USSH ) NAT INST OF HEALTH.
XX
PI   Kinet JP,  Metzger H;
XX
DR   WPI; 1991-346755/47.
DR   N-PSDB; AAQ14736.
XX
PT   DNA coding alpha, beta and gamma-units of ige high affinity receptor -
PT   are used to prepare recombinant polypeptide(s) for treating allergy, drug
PT   screening or monitoring IgE level.
XX
PS   Disclosure; Fig 1; 58pp; English.
XX
CC   A lambda gt11 library was prepared from poly-A RNA isolated from KUB12
CC   cells. Screening was by a cDNA fragment from the rat Fc(epsilon)RI alpha
CC   cDNA corresponding to nucleotides 119-781. Positive clones were subcloned
CC   and sequenced. This amino acid sequence was deduced from the cDNA clone.
CC   (Note: Revised entry submitted to correct the patent number format of US
CC   Government-owned NTIS applications to prevent clashes with ongoing US
CC   granted patent numbers. For further information please visit the Derwent
CC   web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-
CC   MAR-2003 to correct PF field.)
XX
SQ   Sequence 257 AA;
```

```
  Query Match             100.0%;  Score 1264;  DB 2;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-93;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85

Qy         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145

Qy        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205

Qy        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257
```

```
RESULT 5
AAR42336
ID   AAR42336 standard; protein; 257 AA.
XX
AC   AAR42336;
XX
DT   25-MAR-2003  (revised)
DT   21-JUN-1994  (first entry)
XX
DE   Human FceRI alpha.
XX
KW   IgE; immunoglogulin E receptor; beta subunit; basophils; allergy;
KW   aggregation; signal transduction; diagnosis; antagonist.
XX
OS   Homo sapiens.
XX
PN   WO9321317-A1.
XX
PD   28-OCT-1993.
XX
PF   16-APR-1993;   93WO-US003419.
XX
PR   16-APR-1992;   92US-00869933.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX
PI   Kinet JP;
XX
DR   WPI; 1993-351727/44.
DR   N-PSDB; AAQ51020.
XX
PT   Immunoglobulin E receptor human beta sub-unit isolation - using 1st
PT   strand reverse transcripts from human basophils as templates for a
PT   polymerase chain reaction, used to treat and diagnose allergic diseases.
XX
PS   Claim 5; Fig 1; 154pp; English.
XX
CC   The sequence is that of the human FcRI alpha subunit, isolated by using
CC   first strand reverse transcriptase from human basophils by PCR. The gene
CC   and its prod. can be used to identify human beta subuit FceRI inhibitors
CC   (immunoglobulin E receptor) which inhibit the binding of IgE to its
CC   receptor and inhibit the aggragation function of the receptor or the
CC   signal transducing function related to allergic response. Such inhibitors
CC   can be used for the treatment or prevention of allergic disease. See also
CC   AAR42337-42. (Updated on 25-MAR-2003 to correct PN field.)
```

```
XX
SQ   Sequence 257 AA;

  Query Match             100.0%;  Score 1264;  DB 2;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-93;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85

Qy         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145

Qy        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205

Qy        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257


RESULT 6
AAW24066
ID   AAW24066 standard; protein; 257 AA.
XX
AC   AAW24066;
XX
DT   04-FEB-1998  (first entry)
XX
DE   Alpha subunit of human high affinity receptor for IgE (human FcERI).
XX
KW   alpha subunit; human high affinity receptor; IgE; FcERI; antigen;
KW   preformed mediator; histamine; serotonin; leukotriene; IgE level;
KW   allergic condition; therapy; allergic response; drug screening;
KW   DNA probe; diagnostic assay.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /label= signal_peptide
FT   Protein         26. .257
FT                   /label= mature_peptide
FT   Region          26. .204
FT                   /label= extracellular_portion_of_protein
FT   Domain          80. .104
FT                   /label= homologous_domain_1
FT                   /note= "this region is homologous with amino acids 163-
FT                   190"
FT   Domain          163. .190
FT                   /label= homologous_domain_2
FT                   /note= "this region is homologous with amino acids 80-
FT                   104"
FT   Region          205. .224
FT                   /label= transmembrane_segment
FT   Region          225. .257
FT                   /label= cytoplasmic_domain
XX
PN   US5639660-A.
XX
PD   17-JUN-1997.
XX
PF   24-FEB-1988;   88US-00160457.
XX
PR   24-FEB-1988;   88US-00160457.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA   (HOFF ) HOFFMANN LA ROCHE INC.
XX
PI   Kochan JP,  Kinet JP;
XX
DR   WPI; 1997-332052/30.
DR   N-PSDB; AAT85615.
XX
PT   DNA encoding alpha sub-unit of high affinity receptor for immunoglobulin
PT   E - used for producing polypeptide(s) which can be used for therapy or to
PT   prevent allergic responses or in diagnostic and screening assays.
XX
PS   Claim 7; Fig 1A-B; 15pp; English.
XX
CC   This sequence represents the alpha subunit of the human high affinity
CC   receptor for IgE (FcERI). FcERI is found exclusively on mast cells,
CC   basophils and related cells. Aggregation of IgE occupied FcERI by antigen
CC   triggers both the release of of preformed mediators such as histamine and
CC   serotonin, as well as stimulating the synthesis of leukotrienes. It is
CC   the release of these mediators that results in an allergic condition. The
CC   DNA can be used to produce the human FcERI alpha polypeptides which can
CC   be used for therapy or to prevent allergic responses, in drug screening
CC   assays or for monitoring IgE levels in patients. The DNA encoding this
CC   protein can also be used to produce DNA probes useful in diagnostic
CC   assays
XX
SQ   Sequence 257 AA;

  Query Match             100.0%;  Score 1264;  DB 2;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-93;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85

Qy         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145

Qy        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205

Qy        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257


RESULT 7
AAW61190
ID   AAW61190 standard; protein; 257 AA.
XX
AC   AAW61190;
XX
DT   07-OCT-1998  (first entry)
XX
DE   The alpha chain of a Fc epsilon receptor.
XX
KW   Alpha chain; human; Fc epsilon receptor; canine; equine; feline;
KW   immunoglobulin E; IgE; detection; diagnose; allergy; atopic disease;
KW   hyper-IgE syndrome; internal parasitic infection; B cell neoplasia;
KW   flea allergy; heartworm infection.
XX
OS   Homo sapiens.
XX
PN   WO9823964-A1.
XX
PD   04-JUN-1998.
XX
PF   24-NOV-1997;   97WO-US021651.
XX
PR   26-NOV-1996;   96US-00756387.
XX
PA   (HESK-) HESKA CORP.
XX
PI   Frank RG,  Porter JP,  Rushlow KE,  Wassom DL;
```

XX
DR WPI; 1998-322873/28.
DR N-PSDB; AAV36343.
XX
PT Detection of non-human immunoglobulin E - by complex formation with human
PT Fc epsilon receptor, used for, e.g. diagnosis of allergy and atopic
PT disease.
XX
PS Disclosure; Page 37-38; 70pp; English.
XX
CC The present sequence represents the alpha chain of the human Fc epsilon
CC receptor. Detection of canine, equine or feline immunoglobulin E (IgE)
CC comprises reacting isolated human Fc epsilon receptor with the test
CC sample and detecting formation of a IgE-receptor complex. Detection of
CC IgE is used to diagnose allergy, atopic disease, hyper-IgE syndrome,
CC internal parasitic infections or B cell neoplasia, and for measuring
CC effect of treatments. Most particularly flea allergy in dogs and cats is
CC detected, and also heartworm infection
XX
SQ Sequence 257 AA;

Query Match 100.0%; Score 1264; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 5.1e-93;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
Db 26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85

Qy 61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120
Db 86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145

Qy 121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180
Db 146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205

Qy 181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
Db 206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257

RESULT 8
AAB74667
ID AAB74667 standard; protein; 257 AA.
XX
AC AAB74667;
XX
DT 19-JUN-2001 (first entry)
XX
DE Human immunoglobulin E receptor I alpha subunit protein.
XX
KW Human; polymorphism; immunoglobulin E receptor I alpha subunit; IGERA;
KW single nucleotide polymorphism; SNP; allele specific oligonucleotide;
KW immunoassay; detection.
XX
OS Homo sapiens.
XX
PN WO200111010-A2.
XX
PD 15-FEB-2001.
XX
PF 02-AUG-2000; 2000WO-US021097.
XX
PR 09-AUG-1999; 99US-0147860P.
XX
PA (GENA-) GENAISSANCE PHARM INC.
XX
PI Chew A, Denton RR, Duda A, Kliem SE, Lanz EM, Nandabalan K;
PI Stephens JC;
XX
DR WPI; 2001-202766/20.
DR N-PSDB; AAF97964.
XX
PT New polynucleotide for gene therapy, comprises nucleotide polymorphisms
PT in the immunoglobulin E receptor I alpha subunit gene.
XX
PS Claim 10; Fig 3; 99pp; English.
XX
CC The present invention describes an isolated polynucleotide (I) comprising
CC a nucleotide sequence (S) which is a polymorphic variant of a reference
CC sequence for the human immunoglobulin E receptor I alpha subunit (IGERA)
CC gene or its fragment. The polymorphic variant comprises at least one
CC polymorphism selected from guanine (G) at polymorphic site (PS) 1, PS9,
CC PS10 or PS21, cytosine (C) at PS2, PS3, PS6, PS12, PS18 or PS20, adenine
CC (A) at PS5, PS7, PS11, PS13, PS14, PS15, PS19, or PS22 and thymine (T) at
CC PS4, PS8, PS16 or PS17, or (G) at a position corresponding to nucleotide
CC 251, (A) at a position corresponding to nucleotide 302 or 741, and (T) at
CC a position corresponding to nucleotide 530. (I) can be used in gene
CC therapy. (I) is useful for therapeutic purposes. A polypeptide (II)
CC encoded by (I) is useful in drug screening assays and in assays to
CC measure the binding affinity of one or more candidate drugs targeting
CC (II). An antibody (III) to (II) is useful to immunoprecipitate (II) from
CC solution and also reacts with (II) on Western or immunoblots of
CC polyacrylamide gels on membrane supports or substrates. (III) is also
CC useful in immunoassays to detect (II) in biological samples. AAF97965 to
CC AAF98096 represent IGERA allele specific oligonucleotide probes; AAF98097
CC to AAF98140 represent IGERA gene polymorphism detection primers; and
CC AAF98141 to AAF98180 represent IGERA gene PCR primers which are used in
CC the exemplification of the present invention. The present sequence
CC represents the human IGERA protein used in the present invention
XX
SQ Sequence 257 AA;

Query Match 100.0%; Score 1264; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 5.1e-93;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
Db 26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85

Qy 61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120
Db 86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145

Qy 121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180
Db 146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205

Qy 181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
Db 206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257

RESULT 9
AAB31584
ID AAB31584 standard; protein; 257 AA.
XX
AC AAB31584;
XX
DT 30-APR-2001 (first entry)
XX
DE Amino acid sequence of a human Fc epsilon receptor alpha-chain.
XX
KW Fc epsilon receptor; FcepsilonR; immunoglobulin E; IgE; atopic disease;
KW luminescence inducing protein; allergy; hyper IgE syndrome;
KW internal parasite infection; B cell neoplasia.
XX
OS Homo sapiens.
XX
PN WO200104310-A1.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US019070.

```
XX
PR   13-JUL-1999;   99US-0143612P.
PR   02-MAR-2000; 2000US-0186412P.
XX
PA   (HESK-) HESKA CORP.
PA   (PROM-) PROMEGA CORP.
XX
PI   Weber ER,  Wood KV,  Hall MP;
XX
DR   WPI; 2001-103082/11.
DR   N-PSDB; AAF24911.
XX
PT   A fusion protein, comprising an Fc epsilon receptor domain and a
PT   luminescence inducing protein domain that induces a LP substrate to emit
PT   light when contacted with the LP domain, useful for detecting
PT   immunoglobulin (Ig) E.
XX
PS   Claim 16; Page 60; 105pp; English.
XX
CC   The present sequence represents a human Fc epsilon receptor (FcepsilonR)
CC   alpha-chain protein, that binds to immunoglobulin (Ig) E). The FcepsilonR
CC   domain is used to produce a fusion protein, which also comprises a
CC   luminescence inducing protein domain that induces a substrate to emit
CC   light when contacted with the luminescence inducing protein domain. The
CC   fusion protein may be used to detect IgE. It may also be used to identify
CC   a compound capable of inhibiting FcepsilonR protein activity. IgE
CC   antibody production is indicative of diseases such as allergies, atopic
CC   disease, hyper IgE syndrome, internal parasite infections and B cell
CC   neoplasia. Detection of IgE production in an animal following therapy is
CC   indicative of the efficacy of the treatment, for example when using
CC   treatments intended to disrupt IgE production
XX
SQ   Sequence 257 AA;

  Query Match           100.0%;  Score 1264;  DB 4;  Length 257;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-93;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85

Qy         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145

Qy        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205

Qy        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257


RESULT 10
ABG32801
ID   ABG32801 standard; protein; 257 AA.
XX
AC   ABG32801;
XX
DT   29-NOV-2002  (first entry)
XX
DE   Human IgE receptor FcepsilonRIalpha.
XX
KW   Human; IgE; receptor; FcepsilonRIalpha; HSA; human serum albumin;
KW   antiallergic; dermatological; antiinflammatory; antiasthmatic;
KW   IgE binding domain; systemic allergy; IgE-receptor-mediated disorder;
KW   atopic dermatitis; atopic asthma; chronic urticaria.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .25
FT                   /label= Signal_peptide
FT   Protein         26. .257
FT                   /label= Mature_FcepsilonRIalpha
FT   Region          26. .204
FT                   /label= IgE_binding_domain
FT                   /note= "This region is specifically claimed in claim 5"
XX
PN   US6423512-B1.
XX
PD   23-JUL-2002.
XX
PF   21-JUL-1997;   97US-00897956.
XX
PR   26-JUL-1996;   96US-0022689P.
XX
PA   (NOVS ) NOVARTIS AG.
XX
PI   Digan ME,  Lake P,  Gram H;
XX
DR   WPI; 2002-672940/72.
DR   N-PSDB; ABS52959.
XX
PT   New fusion IgE-binding polypeptide, useful for the prevention and
PT   treatment of systemic allergy and/or other IgE-receptor-mediated
PT   disorders such as atopic dermatitis, atopic asthma and chronic urticaria.
XX
PS   Claim 5; Fig 13; 49pp; English.
XX
CC   The invention relates to a new fusion polypeptide or its pharmaceutically
CC   acceptable salt comprises at least one IgE-binding domain fused to at
CC   least one human serum albumin (HSA) component, where the IgE-binding
CC   domain is the sequence (a) defined residues Val26-Leu204 of the protein
CC   sequence appearing as ABG32801, or a truncation at the carboxy terminus
CC   by 1-12 amino acids. Also included are: (1) a fusion polypeptide defined
CC   by residues Val26-Leu978 of the protein appearing as ABG32803; (2) a
CC   polynucleotide sequence encoding the fusion protein; (3) a host cell
CC   transformed with the polynucleotide; (4) a method of preparing the fusion
CC   protein comprising transforming a host cell with a vector comprising a
CC   polynucleotide encoding the fusion polypeptide, expressing the fusion
CC   polypeptide in the cell, and recovering the fusion polypeptide from the
CC   host cell, optionally in the form of its salt; and (5) a vector for
CC   expressing a polynucleotide sequence encoding a fusion polypeptide of
CC   formula (I), (II), (III), (IV), or (V) or its salts ( R_1-L-R_2 (I), R_2-
CC   L-R_1 (II), R_1-L-R_2-L-R_1 (III), R_1-L-R_1-L-R_2 (IV), R_2-L-R_1-L-R_1
CC   (V), where R_1 = the polypeptide (a) or its truncation at the carboxy
CC   terminus by 1-12 amino acids and R_2 = a polypeptide selected from the
CC   sequence defined by residues Asp25-Leu609 the human HSA sequence
CC   appearing as ABG32802, or its truncation at the carboxy terminus by 1-10
CC   amino acids and L = independently a chemical bond, where the vector is
CC   PXMT3-R1a-HAS-R1a). The compositions and methods of the present invention
CC   are useful for the prevention and treatment of systemic allergy and other
CC   IgE-receptor-mediated disorders such as atopic dermatitis, atopic asthma
CC   and chronic urticaria. The IgE-binding polypeptide have a more prolonged
CC   effective serum life, more improved clinical utility in the treatment of
CC   allergy, as well as improved activity in a more efficient and cost-
CC   effective manner. The present sequence is the human IgE receptor
CC   FcepsilonRIalpha used to make the fusion protein of the invention
XX
SQ   Sequence 257 AA;

  Query Match           100.0%;  Score 1264;  DB 5;  Length 257;
  Best Local Similarity  100.0%;  Pred. No. 5.1e-93;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85

Qy         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145
```

```
Qy        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205

Qy        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257
```

RESULT 11
ABO01301
ID ABO01301 standard; protein; 257 AA.
XX
AC ABO01301;
XX
DT 07-AUG-2003 (first entry)
XX
DE Human protein NOV8a.
XX
KW Human; NOVX; cardiomyopathy; atherosclerosis; hypertension;
KW congenital heart defect; prostate cancer; diabetes; metabolic disorder;
KW neoplasm; graft versus host disease; AIDS; bronchial asthma;
KW Crohn's disease; multiple sclerosis; infectious disease; anorexia;
KW cancer-associated cachexia; neurodegenerative disorder;
KW Alzheimer's disease; Parkinson's disease; immune disorder;
KW haematopoietic disorder; dyslipidaemia; wasting disorder; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003023008-A2.
XX
PD 20-MAR-2003.
XX
PF 09-SEP-2002; 2002WO-US028596.
XX
PR 07-SEP-2001; 2001US-0318120P.
PR 07-SEP-2001; 2001US-0318130P.
PR 10-SEP-2001; 2001US-0318430P.
PR 12-SEP-2001; 2001US-0318765P.
PR 17-SEP-2001; 2001US-0322781P.
PR 17-SEP-2001; 2001US-0322816P.
PR 19-SEP-2001; 2001US-0323519P.
PR 20-SEP-2001; 2001US-0323631P.
PR 20-SEP-2001; 2001US-0323636P.
PR 25-SEP-2001; 2001US-0324969P.
PR 25-SEP-2001; 2001US-0325091P.
PR 26-SEP-2001; 2001US-0324990P.
PR 15-FEB-2002; 2002US-0357303P.
PR 28-FEB-2002; 2002US-0360973P.
PR 20-MAR-2002; 2002US-0366131P.
PR 25-MAR-2002; 2002US-0367753P.
PR 02-APR-2002; 2002US-0369479P.
PR 10-MAY-2002; 2002US-0379532P.
PR 17-MAY-2002; 2002US-0381664P.
PR 17-MAY-2002; 2002US-0381672P.
PR 28-MAY-2002; 2002US-0383651P.
PR 29-MAY-2002; 2002US-0384012P.
PR 19-JUN-2002; 2002US-0390155P.
PR 06-SEP-2002; 2002US-00390155.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Zhong M, Li L, Gorman L, Spytek KA, Kekuda R, Taupier RJ;
PI Anderson DW, Vernet CAM, Catterton E, Miller CE, Shenoy SG;
PI Patturajan M, Pena CEA, Tchernev VT, Padigaru M, Gusev VY;
PI Malyankar UM, Burgess CE, Gerlach VL, Casman SJ, Rieger DK;
PI Grosse WM, Smithson G, Peyman JA, Starling G, Rothenberg ME;
PI Larochelle WJ, Shimkets RA, Crabtree J, Rastelli L, Voss EZ;
PI Boldog FL, Edinger SR, Millet I, Macdougall JR, Ellerman K;
PI Chapoval A;
XX
DR WPI; 2003-313246/30.
DR N-PSDB; ACD06182.
XX
PT New polypeptides and polynucleotides having properties related to
PT stimulation of biochemical or physiological responses in a cell or
PT tissue, useful for diagnosing or preventing e.g. atherosclerosis,
PT hypertension, prostate cancer.
XX
PS Claim 2; Page 133; 849pp; English.
XX
CC The invention relates to an isolated polypeptide comprising one of 127
CC sequences (appearing as ABO1288-ABO1414) designated as NOVX, a mature
CC form of NOVX, an amino acid sequence which is at least 95% identical to
CC NOVX or an amino acid sequence comprising one or more conservative
CC substitutions in NOVX. Also included are nucleic acids encoding NOVX
CC proteins, determining the presence or amount of NOVX or NOVX DNA in a
CC sample (by introducing the sample to an antibody that binds
CC immunospecifically to the polypeptide, and determining the presence or
CC amount of antibody bound to the polypeptide), determining the presence of
CC or predisposition to a disease associated with altered levels of
CC expression of NOVX or NOVX DNA in a first mammalian subject, identifying
CC an agent that binds to NOVX, identifying a potential therapeutic agent
CC for treatment of a pathology related to aberrant expression or aberrant
CC physiological interactions of NOVX, screening for a modulator of activity
CC of or of latency or predisposition to a pathology associated with NOVX, a
CC vector comprising NOVX DNA, a cell comprising the vector (used to produce
CC NOVX) and an anti-NOVX antibody. The NOVX nucleic acids and polypeptides
CC are useful as a marker for cell or tissue type, and in diagnosing and
CC treating pathologies, diseases, conditions or disorders associated with
CC NOVX sequences, including cardiomyopathy, atherosclerosis, hypertension,
CC congenital heart defects, prostate cancer, diabetes, metabolic disorders,
CC neoplasm, graft versus host disease, AIDS, bronchial asthma, Crohn's
CC disease, multiple sclerosis, infectious diseases, anorexia, cancer-
CC associated cachexia, neurodegenerative disorders (e.g. Alzheimer's
CC disease or Parkinson's disease), immune disorders, haematopoietic
CC disorders, dyslipidaemias, and wasting disorders associated with chronic
CC diseases. These may also be used to screen for molecules which inhibit or
CC enhance NOVX activity or function, and for detecting specific cell types.
CC These may also be used in chromosome mapping, gene therapy, tissue
CC typing, and in forensic biology. The present sequence represents a NOVX
CC protein
XX
SQ Sequence 257 AA;

```
  Query Match             100.0%;  Score 1264;  DB 6;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-93;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85

Qy         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145

Qy        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205

Qy        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257
```

RESULT 12
ADD48674
ID ADD48674 standard; protein; 257 AA.
XX
AC ADD48674;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human Protein P12319, SEQ ID NO 14381.
XX

KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX
PI Woolf C, D'urso D, Befort K, Costigan M;
XX
DR WPI; 2003-268312/26.
DR GENBANK; P12319.
XX
PT New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
PS Claim 1; Page; 1017pp; English.
XX
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 257 AA;

```
  Query Match             100.0%;  Score 1264;  DB 7;  Length 257;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-93;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85

Qy         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145

Qy        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205

Qy        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 257
```

RESULT 13
AAY96230
ID AAY96230 standard; protein; 260 AA.
XX
AC AAY96230;
XX
DT 11-SEP-2000 (first entry)
XX
DE Human Fc receptor, FcepsilonRIa.
XX
KW Human; Fc receptor; FcepsilonRIa; immunoglobulin; infection;
KW immune response; HIV; IgG; immunosuppressive; antirheumatic;
KW antiinflammatory; AIDS; SLE; multiple myeloma; rheumatoid arthritis;
KW systemic lupus erythematosus; tumour.
XX
OS Homo sapiens.
XX
PN EP1006183-A1.
XX
PD 07-JUN-2000.
XX
PF 03-DEC-1998; 98EP-00122969.
XX
PR 03-DEC-1998; 98EP-00122969.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
DR WPI; 2000-367968/32.
DR N-PSDB; AAA27470.
XX
PT Novel Fc receptor lacking transmembrane domains, a signal peptide, and
PT glycosylation, useful for diagnosing and treating immune disorders and
PT cancer.
XX
PS Disclosure; Page 40-41; 60pp; English.
XX
CC The present sequence is the human Fc receptor, FcepsilonRIa. Fc receptors
CC play an important role in defending the body against infections. First,
CC pathogens are opsonised by serum immunoglobulins. The resulting complex
CC then binds to cells expressing Fc receptors. Upon Fc receptor activation,
CC immune effector pathways are activated, leading to immune response. The
CC present sequence may be modified to produce recombinant versions. The
CC recombinant Fc receptor consist only of the extracellular portion of the
CC receptor and are not glycosylated i.e. they do not have transmembrane
CC domains or signal peptides. The recombinant proteins may be used in
CC immunoassays to determine the immune status of patients with chronic
CC diseases of the immune system, e.g. AIDS, systemic lupus erythematosus
CC (SLE), multiple myeloma (MM), or rheumatoid arthritis. In addition,
CC pharmaceutical compositions containing recombinant proteins may be used
CC to treat or prevent autoimmune diseases, allergies or tumours, especially
CC AIDS, rheumatoid arthritis or MM
XX
SQ Sequence 260 AA;

```
  Query Match             100.0%;  Score 1264;  DB 3;  Length 260;
  Best Local Similarity   100.0%;  Pred. No. 5.2e-93;
  Matches  232;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         29 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 88

Qy         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 148
```

```
Qy        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        149 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 208

Qy        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        209 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 260
```

RESULT 14
AAW48094
ID AAW48094 standard; protein; 257 AA.
XX
AC AAW48094;
XX
DT 20-JUL-1998 (first entry)
XX
DE Human IgE receptor Fc-epsilon-RI alpha chain.
XX
KW Fc-epsilon RI alpha chain; IgE receptor; human serum albumin;
KW fusion protein; allergy; atopic dermatitis; asthma; urticaria; hay fever;
KW eczema; anaphylaxis; gene therapy; diagnosis; transgenic animal.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Peptide   1. .25
FT   /label= Sig_peptide
FT Protein   26. .257
FT   /label= Mat_protein
FT Domain   26. .204
FT   /note= "extracellular domain"
XX
PN WO9804718-A1.
XX
PD 05-FEB-1998.
XX
PF 25-JUL-1997; 97WO-EP004066.
XX
PR 26-JUL-1996; 96US-00690216.
XX
PA (NOVS) NOVARTIS AG.
XX
PI Digan ME, Lake P, Gram H;
XX
DR WPI; 1998-130705/12.
DR N-PSDB; AAV20402.
XX
PT New fusion polypeptide for, e.g. diagnosing allergies - comprises
PT immunoglobulin E-binding domain fused to human serum albumin.
XX
PS Claim 2; Page 44; 77pp; English.
XX
CC This is the amino acid sequence of the dominant form of full-length
CC native human IgE receptor Fc-epsilon RI alpha chain. A claimed fusion
CC protein (FP) comprises an IgE binding domain fused to at least one human
CC serum albumin (HSA) component (see AAW38095), optionally via a peptide
CC linker, and is especially a dimeric FP (see AAW48096) comprising HSA
CC fused, at each of its N- and C-termini, to the extracellular domain of Fc
CC -epsilon RI alpha chain. Also claimed are: nucleic acids encoding the FP
CC (see AAV20404); a vector; a process for preparing the FP; a method of
CC performing gene therapy in humans that comprises removing somatic cells
CC from a patient, genetically modifying them in culture by insertion of a
CC polynucleotide that encodes the FP, and reintroducing the modified cells
CC into the patient so that the FP is expressed by the cells of the patient;
CC and use of the FP in an in vitro diagnostic assay to determine the level
CC of IgE or auto-antibodies to Fc epsilon RI in a sample. The products can
CC be used in the prevention and/or treatment of IgE-mediated allergic
CC diseases and related disorders such as atopic dermatitis, atopic asthma,
CC chronic urticaria, hayfever and eczema. Compared with using IgE binding
CC domain alone, the FP has a longer serum life, and thus greater activity,
CC without a loss of ability to bind serum IgE or circulating auto-
CC antibodies
XX
SQ Sequence 257 AA;

```
  Query Match             99.6%;  Score 1259;  DB 2;  Length 257;
  Best Local Similarity   99.6%;  Pred. No. 1.3e-92;
  Matches  231;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 VPQKPKVSLNPPWNRIFKGENVTLTCNGNNFFEVSSTKWFHNGSLSEETNSSLNIVNAKF 85

Qy         61 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 EDSGEYKCQHQQVNESEPVYLEVFSDWLLLQASAEVVMEGQPLFLRCHGWRNWDVYKVIY 145

Qy        121 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 YKDGEALKYWYENHNISITNATVEDSGTYYCTGKVWQLDYESEPLNITVIKAPREKYWLQ 205

Qy        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPNPNPKNN 257
```

RESULT 15
ADB85536
ID ADB85536 standard; protein; 257 AA.
XX
AC ADB85536;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human immunoglobulin E high affinity receptor alpha subunit protein.
XX
KW alpha subunit; high affinity receptor for immunoglobulin E; FcERI;
KW mast cell; basophil; histamine; serotonin; allergic condition;
KW antiallergic; allergic response; drug screening assay; immunoglobulin E;
KW human.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT Misc-difference 221
FT   /note= "Encoded by GGA"
FT Misc-difference 253
FT   /note= "Encoded by AAC"
XX
PN US6602983-B1.
XX
PD 05-AUG-2003.
XX
PF 22-SEP-1994; 94US-00310902.
XX
PR 24-FEB-1988; 88US-00160457.
PR 30-OCT-1991; 91US-00785127.
PR 29-MAY-1993; 93US-00066640.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kinet JP, Kochan JP;
XX
DR WPI; 2003-669612/63.
DR N-PSDB; ADB85535.
XX
PT New alpha subunit of the human high affinity receptor for immunoglobulin
PT E polypeptides, useful as antagonists to prevent allergic response, as
PT reagents in drug screening assays, or for monitoring immunoglobulin E
PT levels in patients.
XX
PS Claim 1; Fig 1; 9pp; English.
XX
CC This invention relates to a novel purified polypeptide corresponding to
CC the alpha subunit of the human high affinity receptor for immunoglobulin

CC E (FcERI) and the DNA sequence which encodes it. The receptor of the
CC invention is found exclusively on mast cells, basophils and related
CC cells. Activation of the receptor triggers the release of preformed
CC mediators such as histamine and serotonin which may result in allergic
CC conditions. Compounds which modulate FcERI activity may have antiallergic
CC activity. The polypeptide of the invention may be useful as an antagonist
CC for preventing allergic response, as a reagent in drug screening assays,
CC as a therapeutic or for monitoring immunoglobulin E levels in patients.
CC The DNA sequences may be useful for producing the polypeptide or for
CC synthesising cDNA sequences to construct DNA probes used in diagnostic
CC assays. The present sequence is the amino acid sequence of the alpha
CC subunit of the human FcERI receptor of the invention.
XX
SQ Sequence 257 AA;

Query Match 99.0%; Score 1251; DB 7; Length 257;
Best Local Similarity 99.1%; Pred. No. 5.6e-92;
Matches 230; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy        181 FFIPLLVVILFAVDTGLFISTQQQVTFLLKIKRTRKGFRLLNPHPKPNPKNN 232
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